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From: •

Chan, Christina

Sent: To: Subject:

Monday, July 28, 2003 6:04 PM Sullivan, Daniel; STIC-Biotech/ChemLib RE: RUSH Sequence Search for 09834291

## Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message----

Sullivan, Daniel

Sent:

Monday, July 28, 2003 1:45 PM

To:

Chan, Christina

RUSH Sequence Search for 09834291

Subject: Importance: High

Hi Chris-

Could you please approve the following search for an after final amended case.

Please search for the following in the commercial, interference and issued patent databases:

A nucleic acid sequence comprising SEQ ID NO: 1, 2, 3, 4, 6, 15 or 24;

A nucleic acid sequence consisting of SEQ ID NO: 10, 12 or 14

Thank you.

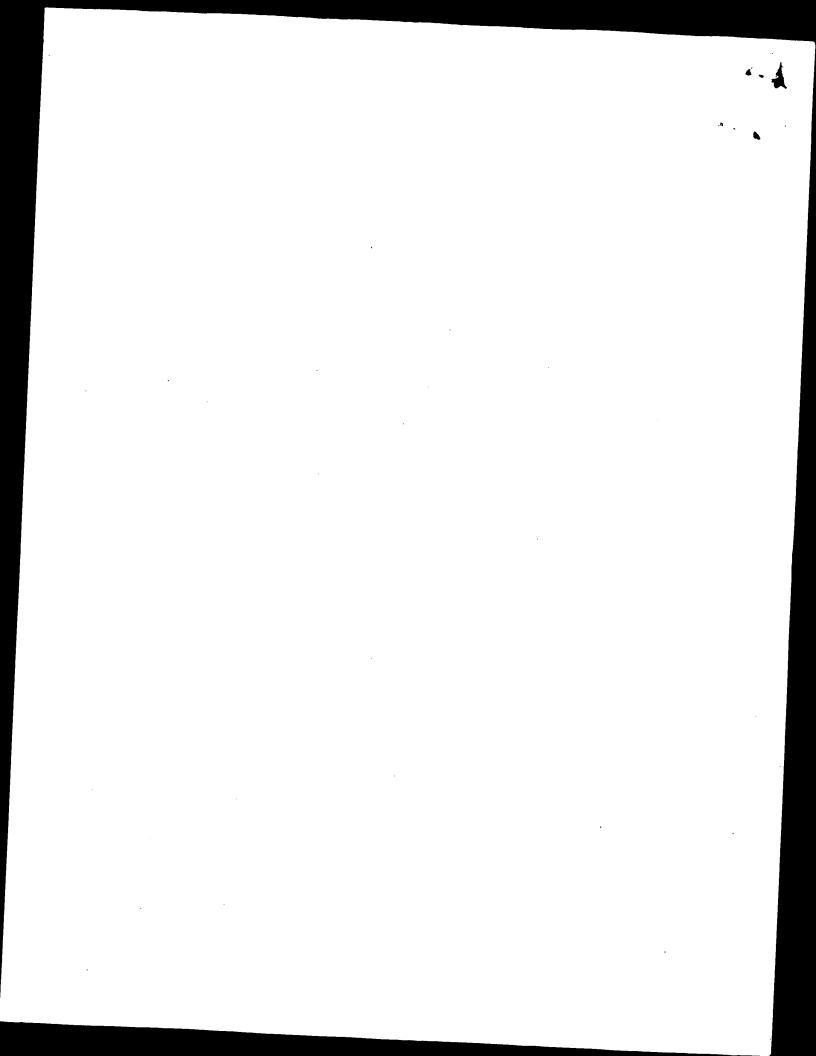
Daniel M. Sullivan Examiner AU 1636 Room: 12D12 Mail Box: 11E12 Tel: 703-305-4448

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Searcher: UTGS
Phone:
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Date Completed: 413 143
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Online time:\_

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
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Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
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Ouestel/Orbit:
DRLink:
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Sequence Sys.:
www/Internet:
Other (specify):



## us-09-834-291-1.rge

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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GORGANISM REFERENCE AUTHORS TITLE 3212 bp Sequence 1 from Patent DE19847779. AX026089 AX026089.1 GI:10187520 wueller-Schilling, M., Krammer, P. and Oren, M. Novel receptor dna useful for identifying apoptosis-modulating Novel receptor dna useful for cancer chemotherapy substances potentially useful for cancer chemotherapy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. DNA linear PAT 16-SEP-2000

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Human DNA sequence from clone RP11-399019 on chromosome 10,
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on Aug 31, 2001 this sequence version replaced gi:14161146.
On Aug 31, 2001 this sequence version replaced gi:n4161146.
On Aug 31, 2001 this sequence assembly data is compared from overlapping clones.

Note that the where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
together with a note of the overlapping clone, as we submit sequences with
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by at least as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; Sw:, in the feature table with their source databases: Em: confirmed by restriction on the WORMPEP in the feature table with their source databases.
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                                                                                                                                                                                                                                                                                                                                        142149 TAAGGGCCCTGAGAAGTTTTGGATTCAGAAAGTTTCAAAATTAAAGTAACCCCAGAATTTT 142208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human was generated from part of bacterial clone Chromosome 10 constructed by the Sanger Centre Chromosome 10 constructed by the Sanger Centre Chromosome 10 constructed information can be found at mapping Group.
                                                                                                                                                                                                               142269 GAĀCTTGĀGGĀTĀĀTTĀĞĀCGTĀCGTGĞGCĀGĀGĞGTĀĞĞĞĞĀĀĞĞĞĞTĀTĞĞCĀTĀĞĀ 142328
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RP11-399019 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                   142329 hadhdcagdaccrroddadcaadararcraadrriahrccidacrcrocratriarta 142388
                                                                                         142389 Acthaccarctriccaateriectiaagertritrigectacartritritritritriatritricaaa
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                             181 TAAGGGCCCTGAGAAGTTTTGGATTAAGAAAGTTTCAAAGTTAAAGTAACCCAGAATTTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TITCCCCAGAACACCAGCATTCATTAGGTGTTCATTCAATAGATTCTTCAAAGGATTCCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGAGGACTCTCAGGAATATGCTGGTAAAATAAAATAACCTTTAGAGATGCCCAAACTGT 60
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/note="Sequence confirmed by AC015461 sequenced by WIBR."
55669 a 36398 c 36888 g 58358 t
                                                541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTTGTCAATTGT 600
                                                                                                                                                                                                                                              GAACTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGGGTATGGCATAGA 360
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661 721 721 721 781 781 781 781 781 781 781 781 781 78	Db  121 AAGGCAAAGAAGTTTGGGGAACAGTATATTATTACCCAACCCTTTGACATTTGCAATTT 240  Qy  181 TAAGGCCCTGAGAAGTTTTGGATTAAGAAAGTTTCAAATTAAAGTAACCCAGAATTT 240  181 TAAGGCCCTGAGAAGTTTTGGATTAAGAAAGTTTCAAATTAAAGTAACCCAGAATTT 240  181 TAAGGCCCTGACAAGTTTTGGATTAAGAAAGTTTCCAAATTAAAGTAACCCAGAATTT 240  181 TAAGGCCCTGACAAGTTTTGGATTAAGAAAGTTTCCAAATTAAAGTAACCCAGAATTT 240  181 TAAGGCCCTGACAAGTTTTGGCCATGATTTTCAAATTAAAGTAACGACATTTT 240  241 CTAAGATTATTGACCATGAAACATATGTCTCCCCACAAAGGACAGAGATATTCCTATTCCTT 300  242 CTAAGATTATTAGACCATGAAACATATGTCTCCCCACAAAGGACACATATTCCTATCTCCTT 300  243 CTAAGACTTGAGGATAATTAGACGTACGTGGGTAAGGGGAAAGGGGGATATGGCATAGA 360  244 CTAAGACTTGAGGATAATTAGACGTACGTGGGTAAGGGGAAAGGGGGATATGGCATAGA 360  245 AAGAACCAGGAACCTTTGGCAAAGATATCTAAGTTTAATTCCTGACTCTGATTTTTTTT

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                                                                 Submitted (28-JUN-1994) Yoshinobu Nakanishi, Kanazawa University, Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa University, Ishikawa 920-0934, Japan (B-mail:nakanaka@dbs.p.kanazawa, Kanazawa, Fax.81-76-234-4480)

Location/Qualifiers
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Nakanishi,Y.
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/product="Fas antigen"
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/mol_type="genomic DNA"
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/clone="pF7"
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Sequence 3 from Patent DE19847779.
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Novel receptor dna useful for identifying apoptosis-modulating
Novel receptor dna useful for cancer chemotherapy
substances potentially useful for cancer chemotherapy
patent: DE 19847779-C 3.03-FEB-2000;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Krammer, P.H.
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                                                                                                                                                                                                                                                                                                                      Submitted (03-SEP-1994) P.H. Krammer,
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                                                                                                                                                                                                                                                                        Heidelberg,
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Tumorimmunology Programm, Im Neuenheimer Feld 280, 6
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X81338.1:145. .253,X81339.1:552. .613,X81339.1:766. .828,
X81340.1:79. .161,X81341.1:255. .279,X81342.1:103. .1757)
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X81338.1:145...253,X81339.1:552...828,X81340.1:79...16:
X81341.1:255...279,X81342.1:103...1757)
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/gene="APT"
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X81338.1:145. .253,X81339.1:552. .613,X81339.1:766. .828,
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                                                                                                                                                                                                                                                                                                     join(1708. .1810,X81336.1:155. .320,X81337.1:146. .283,
X81338.1:145. .253,X81339.1:552. .613,X81339.1:766. .828,
X813340.1:79. .161,X81341.1:255. .279,X81342.1:103. .>1757)
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Matches Query Match

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1466.CTTGAGAAATAAAAACTAAGGGGCCCTCCCTTTTCAGAGCCTTATGGCGCAACATCTGTA 1525
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Cheng, J., Liu, C., Koopman, W.J. and Mountz, J.D.
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RESULT 10

DEFINITION ACCESSION

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/note="chemically treated genomic DNA (Homo sapiens)"
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Epigenomics AG (DE)
      Diagnosis of diseases associated with the immune system Patent: WO 0200928-A 2391 03-JAN-2002,
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                                                                              irtificial sequences.
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AGTCTTTCTCTGAGTGACTCCCAGCAATTAGCCAAGGCTCCLGACCLGA	ACGTCTGTGAGCCTCTCATGTTGCAGCCACAAACAIGCACAGCCTCTAGTTAAATGTTTCGTA 85	TTCAGAGCCTTATGGCGCAACATCTGTACTTTTTTATTATGGTTAATTTTTTAGGA 798	TGGTTAAGTTGTTAGCTTTGTTTTTTTT 731	ATGAGTAACGAAGGACAGGATTA 678	GIILACHAGACHAGAIN 111111111111111111111111111111111111	_	TTCATGCTAAACTACCTAAGAGCTATCTACCG11 CCAAACCAAAACTACTAGTAATAGT 55	ATTIAAATTIAGGTTIAGTAATGATGTTATTATTATATATA	۰. ۱		. :	TATTAATGTGTTATTAATGGGTTGAAITCHAAI 15550000000000000000000000000000000000	AAATGTTAATTGAGAGGAAGTTIGAAAAGGGAAGAGAGGTTGCAGAGTGAG 1137				AGATAAGTTTATTATATTTATAAGATTGGTGGTAAGTGTAGTGATAGATGTAAAATATA +20		ARGGTTGGTACGTTTAGGGTTTTTTTATGGTATTAATAGTTTATTGAAAAGGTGGAATAG 138	TTTTTIA::::::::::::::::::::::::::::::::	TATACCATCCTCTTATCCCACTTCTTTTGIGIC IA I NON I I I I I I I I I I I I I I I I I	29.8%; SCULE 70.00.8.8e-217; Indels 5; Gaps 3; Indels 5; Gaps 3; Conservative 0; Mismatches 371; Indels 5; Gaps 3;	3	11608 [organism="synthetic construct"   /organism="synthetic construct"   /organism="synthetic construct"   /moll_type="genomic DNA" /note="chemically treated genomic DNA (Homo sapiens)" /note="chemically treated genomic DNA (Homo sapiens)" /note="chemically treated genomic DNA (Homo sapiens)"

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                                                                                                                                                                                                                                                720 bp
Sequence 2 from Patent DE19847779.
AX026090
                                                                                          Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating
Novel receptor dna useful for cancer chemotherapy
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 2 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
                                                                                                                                                                                                                                      AX026090.1 GI:10187521
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                            Homo sapiens (human)
                    142 a
                  /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/81 c 216 g 18
                                                                                 Location/Qualifiers
                                                          /organism="Homo sapiens"
                               181 t
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22.2%; Score 713; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.3e-158;
Matches 713; Conservative 0; Mismatches 0; Indels
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Kuppers, R., Ne, P., Jungnickel, B., Diehl, V., Rajewsky, K. a Somatic mutations of the CD95 gene in human B cells as a Unpublished
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                                     Muschen, M., Re,D., Jungnickel,B., Diehl,V., Rajewsky,K. and
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                              Homo sapiens (human)
                                                                                                                          AJ279012.1 GI:13539240
Apo-1 Fas; CD95 antigen; CD95 gene.
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                                                                                                                                                                        Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon AJ279012
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Homo sapiens partial CD95 gene for CD95 antigen (Apo-1 Fas), exon
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VERSION
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AJ279013
AJ279013.1 GI:13539242
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/product="CD95 antigen"
/protein_id="CAC35539.1"
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Query Match Best Local Similarity 99.4%; Pred. N. Matches 698; Conservative 0; Mism.  Qy 1946 GAGGCTTCCTTCCCATCCTCCTGACCAC	// Sene="CD95" // Standard_name="Apo-1 Fas' // codon_start=1 // product="CD95 antigen" // protein_id="CAC35541.1" // protein_id="CAC35541.1" // db_xref="GI:13539243" // translation="MLGIWTLLPLV" // translation="MLGIWTLLPLV" // gene="CD95" // standard_name="Apo-1 Fas" // number=1 // DASE COUNT // 108 a 198 c 263 g 133	/gene="CD95" /standard_name="Apo- /number=1 /number=1 /number=1 /number=1 /number=1 /standard_name="Apo- /standard_name="Apo- /standard_name="Apo- /standard_name="Apo- /standard_name="Apo- /standard_name="Apo- /standard_name="Apo-	/organism="Homo sapiens" /mol_type="genomic DNA" /db xref="taxon:9606" /cell_type="Reed-Sternberg c /note="Hodgkin's disease tis gene 1702 /gene="CD95" exon /l313	3 (base Muschen, Direct & Submitte Institut Koeln, & Related	Mammalia; Eutheria; Prin Mammalia; Eutheria; Prin Muschen,M., Re,D., Jungr Kuppers,R. Somatic mutations of the side-effect of the germi cupublished Unpublished Muschen,M., Re,D., Braun Kuppers,R. and Rajewsky, Somatic mutations of the Cells Unpublished
Similarity 21.7%; Score 695.6; DB 9; Length 702;  8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  GAGGCTTCCCTTCCCATCCTCCTGACCACCGGGGCTTTTCGTGAGCTCGTGATCTCG 2005  [	-1 Fas" 11.1" 11.1" 11.1" 11.1	-1 Fas"	piens" DNA" D6" ernberg cells" (sease tissue-polymorphic allele (+337)"	Muschen M., Department of Immunology, LFI E4 R705, Joseph-Stelzmann-Str. 9, 50931 58 X89101 AJ279011 AJ279012.	cdata; Craniata; Vertebrata; Euteleostomi; nates; Catarrhini; Hominidae; Homo. Nickel,B., Diehl,V., Rajewsky,K. and CD95 gene in human B cells as a nal center reaction CD95 gene in Hodgkin- and Reed-Sternberg

Search Job tim	g d	Q B	QQ DB	Ş	D <sub>D</sub>	Ś	Db ·	Ş	В	Ş	DЬ	Ş	당	γQ
ch completed: August 1, 2003, 17:32:41 time : 12570.1 secs		601 CTGCGCTCCACGTTGAAGGCGAAGTCTGGGA 2605	541 TGATGCGAAGTGCTGACCCCGGCGGCGGCGCACCCCCCGGAGACCA 2545  2546 CTGCGCTCCACGTTGACGTGGGCAGGCGCGCGCAGGCGCGCTCCTCGGAGACCA 600	2486 TGATGCGAAGTGCTGATCCCGGTGGGGAGGACGTGGAGGACTTGCTTTTTTTT			μ ,	2366 GGGCACCTTGCCTGCTGCTGCTGCTGCGGGGGGGGGGGG		2306 GATAGGCAAAGTCCCCCCCCCCCCCCCCCCCCCCCCCCC		2246 TCCTACCTCTGGATCATCATCTCTCTCTCTCTCTCTCTCT		2186 GTTGGGGAAGCTCTTTCACTTCGGAGGATTGCTTCAACAACAACATTCCTTCATCATCATTCCTTCATCAT

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OM nucleic - nucleic search, using sw model
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793 bp mRNA linear EST 25-SEP-2001
BI763679 ROMA Clone IMAGE:5189752 5',
603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The J.M.A.G.E. Consortium (CONSTRUCTION OF THE CONSTRUCTION OF THE CONSTR
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                            Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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AN056275 zf53g03 s
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                                   2920 GTCACACAGAAAAGGAAACTGCCTTGTCTCCCCTTTCCGGGAATTCTCTCTTTTAAGACTGTA 2979
                                                                                                                                                                   2861 TCGAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTT-TTTATT 2919
136 Greacacacaaaaaaaaaacreecrrerererecerrecesaarrerererraaaacrera 77
                                                                                                                                                                                                                                                                                                  2741 AGCCTACAGCCTTCAGAACACATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAAT 2800
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                                                                                                                                                                                                                                                                                                                                                                                               316 AGCCTGCAGCCTTCAGAACAGATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAAT
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                                                                                                                               TCGĀĀĀĀĀĠTTĀTĀTGĠĠĠĠĠĊŦĠĀĀTGĀĠĊŦŤĊŦĠĠĀĠĠĊŦŤĠŦŤŦĀĊĊĠŦŦŤĊŦŦŦĀŤŤ 137
                                                                                                                                                                                                                                                           AGGTGGGCTTGGGCGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGCT 437
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/clone lib="NIH MGC 116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
stomachs, 62 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
destroyed upon cloning). Average insert size is theert size range 1-3 kb. Library is normalized and
sinsert size range 1-3 kb. Library is normalized and
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
183 a 265 c 208 g 137 t
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/clone="IMAGE:5189752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/mol_type="mRNA"
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97.48;
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                                                                                                                                                                                                                                                                                             Local
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754 GCAGAGATAATACAGAGAATGCCCATATACCATCCTCCTTATCCCACTTCTTTTTGTGTC 813
                                                                                                        694 ACATTITITTATTTAAATGAACTTTTCATTTTGGAATAGTTTTAGGATTTCAAAAAATTT 753
                                                                                                                                                                                                                                                                               Similarity
                                                                  ACATTTTTTATTTAAATGAACTTTTCATTTTGGAATAGTTTTAGGATTTCAAAAAATTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -4oml3 fwd. ET from Amersham
High quality sequence steps: 459.
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1 (bases 1 to 467)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, M., Lennon, G., Marra, M., Martin, Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., WashU-RCI human EST project
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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2319h02.s1 Soares fetal liver_spleen_INFLS_SI Homo sapiens CDNA
nage:45077I 3', mRNA sequence.
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314 286 1810
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/db_xref="taxon:9606"
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                                                                                                                                                                                                      14.1%; Score 453.4; DB 9; Length 467; 99.6%; Pred. No. 1.1e-67; tive 0; Mismatches 1; Indels 1
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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Clone distribution: MGC clone distribution.
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plate: LLAM12796 row: 1 column: 21
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/clone_lib="NIH_MGC_ll8" (Site_1: Not1; Site_2: EcoRV /clone_lib="NOTM-SPORTG; Site_1: Not1; Site_2: EcoRV /note="Vector: pCMV-SPORTG; Site_1: Not1; Site_2: EcoRV /note="Vector: pCMV-SPORTG; Library is oligo-dT primed (destroyed) and library is oligo-dT primed non-activated adult donors. Library is oligo-dT primed non-activated adult donors. Library is destroyed upon and directionally cloned (EcoRV site is destroyed upon and electronally cloned 1.7 kb, insert size range cloning). Average insert size 1.7 kb, insert size range cloning). Average and was constructed by C. Gruber full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:5756324"
                                                                                                                                                                                                                                                                                                          tissue_type="leukocyte"
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Genoscope - Centre Cedex - France
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                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="pLACENTA"
/clone_Tib="Homo sapiens pLACENTA"
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pred. No. 3.1e-58;
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Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2649 CGGAACTCCTGGACAAGCCCTGACAAGCCAAGCCAAAGGTCCGCTCCGG 2697
                                                                                                    Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2589 GAAGCGGAAGTCTGGGAAGCTTTAGGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAG 2648
                                                                                                                                                                                               Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, S., Maguire, L., Waterston, C., Taagaraishvili, R., Ronko, I., Kennedy
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                                                                                                                                                                                                                                                                                                Sarcocystidae; Toxoplasma.
1 (bases 1 to 506)
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506 bp mRNA linear EST 11-MAY-2001 T9ESTzya24901.yl T9VEG118 Tachyzoite CDNA Library Toxoplasma gondii CDNA clone T9ESTzya24901.yl 5' similar to TR:QG3030 Q63030 RAT
                                                                                                                                                                                                                                                                                                        Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
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Library was not normalized. The pCMVSPORT 6 vector.
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99.0%;
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                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                  BX472931.1 GI:31667185
                                                                                                                                                                                                                                                                                                                  DKFZp686B09151 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
BX472931
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/note="TyVEG118 Tachyzoite cDNA Library"
: This library was constructed by Keliang Tang, Robert
cole, and L. David Sibley at Washington University. cDNAs
size-selected and directionally cloned into the Uni-ZAP XR
lambda vector (Stratagene). The primary library was mass
excised as phagemids and rescued in SOLR cells. The
plasmid library was recovered from the SOLR cells and
inc. Jeor sequencing. WARNING: This library may contain
a small percentage contaminants from human fibroblast
secols."
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/clone="TgESTzya24901.y1"
/dev_stage="Tachyzoite"
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/mol_type="mRNA"
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99.7%;
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0; Mismatches I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST (Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.) unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sl sequence also available. is available at the RZPD in Berlin This clone (DKFZp686B99151) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405; please contact the RZPD: Ressourcenzentrum, GERWANY; Email: clone@rzpd.de. Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2882 TGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATTGTCACACAGAAAAGGAAACTGC 2941
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602185634F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309953 5',
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     Homo sapiens (human)
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/note="vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="human skeletal muscle"
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Mammalia; 1 to 599)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue procurement: Linehan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2349 GCGGCAGCGCGCACGCGGCACCTGGGAGCGGCGGCTGCTGCGGGAGGCGTTGGAGAC 2408
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/lab_host="pH10B (phage-resistant)"
/lab_host="NIH_MGC_45"
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pred. No. 2.6
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cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
End distribution: MGC clone distribution can be http://image.llnl.gov
http://image.llnl.gov
High quality sequence start: 33
High quality sequence stop: 174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                        5'-CACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selection for average insert length 1.87 kb. This is a property non-amplified Library constructed by Library constructed by Life College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Lupaki sciatic nerve"
/note="Vector: PCMV-SPORTS (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
5'-TCGACCCACGCGTCCG_3' and
f'-TCGACCCACGCGTCCG_3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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/mol type="mRNA"
/db_xref="taxon:9606"
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/GELL 'LINE="JOSHC"
// Ab host="Top10F""
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// Clome_lib="Inl2DSHC(081"
// Clome_lib="Inl2DSHC(081"
// Site_2: Not!; The poly (A) + RNA was dephosphorylated with sacterial alkaline phosphatase (BAP) and then decapped for the stand constant of the first intact mRNA was ligated with DNA.RNA linker including priming with dT-tailed vector. The dT-tailed vector was circularized with E. coli DNA ligase and the first adjusted to have about 60mt. The cDNA vector was converted to a DNA strand by Okayama-Berg method. The cDNA transformation of obtained cDNA vectors were used for transformation of full-length enriched cDNA library, by electroporation method. The cDNA this method are library, the abundant cDNAs were selected and are library, the abundant cDNAs were selected and mpthere constructed by this method are products were used as template for primer including Tromotor as 5, primer and N(dT)14 as 3, primer. The pCR reaction. The synthesized RNA by in vitzo transcription liberary and incubated with avoidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA incompetent form original libraries were constructed by the subtracted cDNA incompetent constructed by the subtracted cDNA promotor as 5 primer and N(dT)14 as 3, primer. The PCR reaction. The synthesized RNA probes were hybridized with libraries were constructed by transformation of incompetent cells E. coli ToplOF, with
                                                            92 a
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Plate: 7 row: E column: 08
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Korea Research Institute of Bioscience & Biotechnology
Tel: +82-42-860-4409
Fax: +82-42-860-4409
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Vim, V., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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1 (bases 1 to 1140)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
plate: LLAM10237 row: i column: 24
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z. Insight into hepatocellular carcinogenesis at transcriptome level Insight into hepatocellular carcinogenesis of hepatocellular carcinoma by comparing gene expression profiles of hepatocellular carcinoma by comparing sene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV695647 GKC Homo sapiens cDNA clone GKCFCD11 5', mRNA sequence.
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1 (bases 1 to 617)
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Sis Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
                                                                                                                                                                                                                                                                                  Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualiflers
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/dev_stage="Adult"
                                              /clone="GKCFCD11"
/tissue_type="hepatocellular carcinoma"
                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                   High quality sequence stop: 394.
Location/Qualifiers
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                                                                                                                                             Email: yongsung@mail.kribb.re.kr
Plate: 11 row: C column: 12
                                                                                                                                                                               Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                    Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 394)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., vim, v.c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GAAGCGGAAGTCTGGGAAGCTTTAGGGTCGCTGGAGGGGGACCCCCGGTTGG 1
                                                                                                                                                                              Fax: +82-42-860-4409
                                                                                                                                                                                                                                                  Contact: Kim YS
                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                    21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L5HLK1s1-11-C12"
clone_lib="L5HLK1s1"
           /cell_line="HLK-1"
/lab_host="Top10F'"
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Pred. No. 3.1e-46;
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Matches

RESULT 13 AA058563

Snoo

AA058563

2155b04.s1 Soares retina N2b4HR Homo sapiens cDNA clone AAAARSK5

EST 02-FEB-1997

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SOURCE VERSION ACCESSION DEFINITION

ORGANISM

Homo sapiens (human)

AA058563.1 GI:1551370

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**KEYWORDS** 

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15 GAAGCGGAAGTCT 3
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                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped intact mRNA was ligated with DNA-RNA linker including strand cDNA was synthesized from oilgo dI-selected mRNA was synthesized from oilgo dI-selected mRNA by adjusted to have about 60nt. The cDNA vector was circularized with E. coil DNA ligase after digestion of converted to a DNA strand by Okayama-Berg method. The competent cells E. coil Toplor by electroporation method. The competent cells E. coil Toplor by electroporation of first competent cells E. coil Toplor by electroporation dilbrary, the abundant cDNAs were selected and amplified by Dromotor as 5' primer and N(dT)14 as 3' primer. The PCR biotinylated single stranded RNA by in vitro transcription antisense single stranded cDNAs probes were hybridized with hiberary and incubated with avidin-gel. After removing libraries were constructed by the method are single stranded cDNAs probes were hybridized with probes were hybridized with hiberary and incubated with avidin-gel. After removing libraries were constructed by transformation of the electroporation method."
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This clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact the India clone is available royalty-free through LLNL; contact through India clone is available royalty-free through LLNL; contact through LLNL; contact through LLNL; contact through India clone is available royalty-free through India clone is available royalty-
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/db_xref="taxon:9606"
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Fax: 314 286 1810
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AA056275 577 bp mRNA linear EST 2153903.sl Soares retina N2b4HR Homo sapiens cDNA clone
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
Hillier,L., Clark,N., Dubuque,T., Lennon,G., Marra,M., Parsons,J.,
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
R., R., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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3040 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG 3099
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
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//note="Organ: eye; Vector: pT773D (Pharmacia) with a /note-"Organ: eye; Vector: pT773D (Pharmacia) with a /note-"Organ: eye; Vector: pT773D (Pharmacia) with a Not I; Site 2: ECO RI; 1st /noted cDNA was primed with a Not I - oligo(dT) primer [5']
strand cDNA was primed with a Not I igated to Eco RI retranded cDNA was size selected, ligated to Eco RI double-stranded cDNA was size selected, ligated to Eco RI double-stranded cloned into adapters (Pharmacia), digested with Not I and cloned into adapters (Pharmacia), The retinas were obtained from a 55 year old (Pharmacia) and total cellular poly(A) + RNA was extracted 6 (Caucasian and total cellular poly(A) + RNA was extracted 6 (Caucasian and total cellular poly(A) + RNA was extracted by rowided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. Ph.D. from the provided by Roderick R. McInnes M.D. 
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/lab_host="DH10B (ampicillin resistant)"
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 893 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 471.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiller, L., Lemon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, M., DuBuque, T., Favello, A., Gish, W., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Morres, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Underwood, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Generation and analysis of 280,000 human expressed sequence tags 97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 Griritgádádagriccircegricagadagrigeciágarigagriadarcanag 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TACTOGTTOCOCACOGCACAGAACCOGGNGCOTATTATTGGCCAAGAAACTTGAGCAGCCT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGG 180
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
                   131
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2f49ell.81 Soares retina N2b4HR Homo sapiens cDNA clone
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    /clone="IMAGE:380300"
                                                                                                                                                                                                                                                                                                                         /db_xref="GDB:1288557"
                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
|mol_type="mRNA"
5 others
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DЬ	Ş	DЬ	Ś	DЬ	γŞ	DЬ	Ş	Dъ	γQ	Ques Best Matc
	3160 GTTTTGAAAACTTCCTTCCTTTTTTTTTTTTTTTTTTTT	181 TACTCGTTCCCACCGCAGAAACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCT 3159	3100 TACTCGTTCCCACCGCACACACACACACACACACACACAC	121 CCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGGGGTTGGTGG 3099	3040 CCCTTTCTTAGCTTCTAGCTAGCTAGCTAGCTAGCTAGCT	61 AGTCGCCTGAGTGGTTTCATTTTTTTTTTTTTTTTTTTT	2980 AGTCGCTGCCTGAGTGCTTTTAAGACTGTA 60	1 GTCACAGAAAAAAGAAACTGCCTTCCTTCTCTCTCTCTCT	2920 GTCACAGAAAAGGAAACTGCCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	

Search completed: August 1, 2003, 20:42:50 Job time : 11002.1 secs

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
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3212
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Copyright (c) 1993 - 2003 Compugen Ltd.
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## Result No. 1536.8 2143.4 961 957.4 287.4 262.8 252 252 Score Match Query 66.7 47.8 29.9 29.8 8.9 8.2 7.8 Length DB ID 2165 1608 1608 1608 1608 259 266 2551 2551 24 27 24 21 21 21 21 24 ABN79677 AAT34162 ABL34419 ABL34418 AAC98177 AAZ88700 AAC61798 ABV94152 SUMMARIES Description sequence #1 used t Fas promoter regio Human immune syste Human immune syste Human colon cancer Human CD95 recepto DNA encoding a hum Breast carcinoma r

ARSULANTO	110 1111 1111 1111 1111 1111 1111 1111
T 1 ABN79677 standard; DNA; ABN79677; ABN79677; ABN79677; 29-JUL-2002 (first enti Sequence #1 used to gene Human; immunosuppressiv cytostatic; vasotropic; ds; Fas.  Homo sapiens.  Key CDS /*tag= /produc US2002004490-Al. 10-JAN-2002. 09-MAR-2001; 2001US-08 12-APR-1999; 99US-02 18-SEP-2000; 2000US-06	252 7.8 2551 24 252 7.8 2551 25 226 7.0 2471 16 226 7.0 2534 19 226 7.0 2534 19 226 7.0 2534 19 226 7.0 2534 19 227 7.0 2634 19 228 7.0 2534 19 229 7.0 2534 19 220 7.0 2534 19 221 7.0 2632 12 221 7.0 2632 12 222 7.0 2632 12 223 7.0 2632 12 224 7.0 2632 12 225 7.0 2632 12 227 7.0 2632 12 228 7.0 2632 12 229 7.
see target oligonu antiinflammatory; epatitis; cancer;	NN79588 NN79588 NX10416 2283782 AQ23878 AQ23959 AQ29959 AQ21094 AQ402280 AQ402280 AQ402280 AQ402280 AQ402280 AQ402280 AQ402280 AQ402280 AQ402280 AQ402863 AQ
cleotides. hepatotropic; allograft rejection; allografe rejection; get oligonucleotides	Human Fas locus HS DNA encoding prote Fas-delta-FM cDNA. Soluble Fas recept Human cell surface plasmid pp58 conty hras coding sequen fas cDNA. Mammali Human Pas antigen Human lung tumour cDNA encoding L801 Human lung cancer Lung cancer therap cDNA encoding L801 Human lung cancer Human lung cancer Human lung cancer Lung cancer therap cDNA encoding Colon EP-892047 Seq ID 4 Human cDNA differe Genomic DNA differe Human Fas soluble Breatt cancer rela Kidney cancer rela Human Fas soluble Human Fas soluble Breatt cancer soluble Human Fas soluble Brasel Cancer Soluble

MARCUSSON E

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This invention relates to an antisense compound encoding Fas, CC Fas ligand, or Fas associated protein-1 (Fap-1). The inhibition of CC Fas mediated signalling is thought to be immunosuppressive, antiinflammatory, hepatotropic, cytostatic and vasotropic.

CC Antisense oligonucleotides were designed to target human Fas.

CC Oligonucleotides were synthesised as chimeric oligonucleotides for treating an animal having an autoimmune or complete the control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 2158; Conservative
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                                                  927 GGTGGTAAGTGCAGTGACAGATGCAAAACACAGGGTGATGGAAAGCCCTCAGGAGGGTAA 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand or Fas associated protein-1 is useful for inhibiting expression of Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating
                                                                                                               421 TĠĠĊĀĊTĀĀĊĀĠŦĊŦĀĊŦĠĀĀĀĠĠŦĠĠĀĀĊĀĠĀĠĀĊĀĀĠĊĊŦĀŦĊĀĀĊĀĊĊŦĀĊĀĀĠĀĊŤ 480
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                                                                                                                                         867 TGGCACTAACAGTCTACTGAAAGGTGGAACAGAGACAAGCCTATCAACACCTACAAGACT 926
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(MARC/) MARCUSSON
(WYAT/) WYATT T
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                         2006 CGCAAGAGTGACACACAGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACG 2065
                                                                                                     1946 GAGGCTTCCTTCCCATCCTCCTGACCACCGGGGCTTTTCGTGAGCTCGTCTCTGATCTCG 2005
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                                                                            GAGGCTTCCCTTCCCATCCTCGACCACCGGGGCTTTTCGTGAGCTCGTCTCTGATCTCG 1560
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                                                                                                                                                                                                                                                                                                           661 TÄÄTTGGGÄÄGGGGÄGÄGÄGÄGTTĞCÄĞÄĞTGÄĞĞTĞCÄĞÄĞCTTĞĞTĞĞÄĞGATĞĞTĞĞA
                                                                                                                                                                                                                                                                                                                                       TCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGCCACTGCAGGAACGCCCCGGGACAGGA 1825
                                                                                                                                                                                                                                                                                                                                                                                       CCTČCČČÁŘČTŤCČČÁĞĠŤTGAŘČŤAČŘĠČÁĞÁŘĠČĆŤŤŤÁĞÁŘÁĞĠĠČÁĞĠAĞĠŠČČĠĠĆ
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                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "Fas gene promoter region"
                         /function= Myb transcription factor binding site /note= "claim 9" 349.353
                                                                                                                                                                                                                                                           168..174
                                                                                                                                                                                                                                                                             /function= GF1 transcription factor binding site /note=_"Claim 7"
                                                                                                                                                                                                                                                                                                                                                                                         147..151
                                                                                                                                                                 272..276
                                                                                                                                                                                   function= EBP20 transcription factor binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                     AX A novel DNA segment (AAT34162) has an isolated sequence region code fixed as the Fas gene promoter region. This includes a number code defined as the Fas gene promoter region. This includes a number code fixed as the Fas gene promoter region. The protein leader peptide code is also included. The DNA segment was isolated from a human fas cDNA code is also included. The DNA segment was isolated from a human fas cDNA code is also included. The DNA segment was isolated from a human fas cDNA code is also included. The DNA segment was isolated from a human fas cDNA code is also included. The DNA segment was isolated from a human fas cDNA code is also included the replacement of the placement of the placement of the placement of the placement of the structural code corresponding to nt 23-346. It can be combined with a structural placement of the promoter region can be used corresponding to nt 23-346. The promoter region can be used complete that the gene is under the transcriptional control of the code gene so that the gene is under the transcriptional control of the corresponding to nt 23-346. The promoter region can be used complete so that the gene expression, e.g. in tumour or immune cells, as code is also included apoptosis disorders such as complete the transcriptions of treating Fas-mediated apoptosis disorders such as code maingnancies and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_bind
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                                                                                                                                                                                                                                                                                               Query Match 47.8%; Score 1536.8; DB 17; Length 1608; Best Local Similarity 98.6%; Pred. NO. 0; Best Local Similarity 0; Mismatches 17; Indels 5; Conservative 0; Mismatches 1582; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Fas gene promoter region - used for heterologous protein expression and for developing products for treating Fas-mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 2; 123pp; English.
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                                                                                                                                                                                767 AGAGAATGCCCATATACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCA 826
                                                                                                                   827 GAGTGTGCGCACGAGGCTGGCACGCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGA 886
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/note= "claim 8"
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/note= "claim 5"
1037..1043
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Claim 1; SEQ ID NO 2392; 32pp + Sequence Listing; German.
                                                        Nucleic acid comprising fragment of chemically modified gene, useful cytosine methylation -
                                                                                                                                                                                                                                                                         WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG.
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01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipocriatic; antimetery; cancer; eye disease; arteriosclerosis; anaemia; neurofibromatosis; rheumatoid arthritis; psoriasis; epilepsy; anemonia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; anaemia; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; anaemia; acute myeloid sease; rheumatoid arthritis; psoriasis; bowel disease;
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1606 AAATGCCCCGCAAGTCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCA 1665
                                                                                      1546 TCCATTCCAGAAACGTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCCAGTC 1605
                                                                                                                                                                                                                          The present sequence is a gene of the invention.
                                                                                                                                              882 ADAČČĆTŠĆCTŤTTCÁDÁAČĆCTÁTAAČGCÁÁČÁTČTATÁČTŤŤŤTČÁTÁTAAŤŤÁÁČŤA 823
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                                                                  29.9%; Score 961; DB 24; 76.6%; Pred. No. 2.5e-251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 2391.
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                                                                                                                                                                                                          antiarteriosclerotic; antianaemi; cytostatic; nootropic; antiarteriosclerotic; antiantecio; cytostatic; nootropic; neuroprotective; anti-HIV; anticomvulsant; ophthalmological; natirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirheumatic; cancer; eye disease; arteriosclerosis; anaemia; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             642 AAACTACAACAAAAACCTTTAAAAAAAAAACAAAAAACCGACTCTCGAAATCCTCACCTAAA 583
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                                                                                         Homo sapiens.
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  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences and the diagnosis and treatment of immune system disorders, macular degeneration, arteriosclerosis, anaemia, neovascular glaucoma and rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1608 BP; 398 A; 51 C; 423 G; 736 T; 0 other;
                                                       1258 TTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCCAAAGCAATAGTGACTTTGAACAGT 1317
                                                                                                      1198 AACTGCATCCAAATTCAGGTTCAGTAATGATGTCATTATCCAAACATACCTTCTGTAAAA 1257
                                        499 TTTÁTGTTÁÁÁTTÁTTTÁÁGÁGTTÁTTTÁTCGTTTTÁÁGGTÁÁTÁGTGÁTTTTGÁÁTTÁGT
                                                                                                                                                   1138 GTGCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2391; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified gene, useful conditions and treatment of diseases associated with abnormal
                                                                                     1078 TATTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAG 1137
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                                                                                                                                                                                                                                                1018 CAGAAGAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGT 1077
                                                                                                                                                                                319 TATTAATGTGTTATTAATGGGTTGAATTTAATTGGGAAGGGGAGAGAGGGTTGTAGAGTGAG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                             259 TAGAÁGAÁÁÁTGTTÁÁTTGÁGÁGGÁÁGTTTGÁÁGGÁTGÁÁTÁGTGGGTTÁÁGTÁÁÁGGGT 318
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                                                                                                                                                                                                                                                                            959 GGGTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGG-CCCAACAGGCTC 1017
                                                                                                                                                                                                                                                                                                                          139 AGÁTAAGTTTATTAÁTATTTÁTAÁGÁTTGGTGGTAÁGTGTÁGTGÁTAGATGTÁAÁÁTÁTÁ 198
                                                                                                                                                                                                                                                                                                                                             899 AGACAAGCCTATCAACACCCTACAAGACTGGTGGTGAGTGCAGTGACAGATGCAAAACACA 958
                                                                                                                                                                                                                                                                                                                                                                                            839 AAGGCTGGCACGCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAG 898
                                                                                                                                                                                                                                                                                                                                                                                                                                    779 TATACCATCCTCCTTATCCCACTTCTTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCAC 838
                                                                                                                                                                                                                                                                                                                                                                       79 AAGGTTGGTACGTTTAGGGTTTTTTTTATGGTATTAATAGTTTATTGAAAGGTGGAATAG 138
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                                              2338 GCGGGATTGCGGCGGCAGCGGCGCACGCGGG 2368
                                                              1458 ÍTAÁRÁATTÁÍGFRÁGGRÁFTTÍGGÁTTTÍTTTÁTTTTÓGRÁGTTTÍTTTTTTTTTTÁGGÁG 1517
                                                                                                                               2218 TCAACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTGATCCCTCTCCTGCCGGG 2277
                                                                                                                                                          2158 GCGGGTTGGTGGACCCGCTCAGTACGGAGGTTGGGGAAGCTCTTTCACTTCGGAGGATTGC 2217
                                                                                                                                                                                                       2098 TGGCACGGAACACACCCTGAGGCCAGGCCTGGCTGCCCAGGCGGAGCTGCCTCTTCTCCC 2157
                                                                                                                                                                                                                                                    1278 TTTTGGGGAGTGAGGGAÁGGGGTTTACGAGTGATTTGGTTGGÁGTTTTAGGGGGGGGTAT 1337
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                                                                                                                                                                                                                                                                                                 1218 GTŤTŤŤĊĠŦĠĀĠŦŤĊĠŤŦŤŦŤĠĀŤŦŤĊĠĊĠŦĀĀĠĀĠŤĠĀŦĀŦĀĠĠŤĠŤŤŦĀĀĀĠĀĊĠT 1277
                                                                                                                                                                                                                                                                                                                    1978 GCTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGC 2037
                                                                                                                                                                                                                                                                                                                                              1098 TTŤTÁTTTTĠĀTTŤTŤTTTTTŤTTTŤATTĆĠĆĠĆĠTĀĠĠTTĀĀĠŤŤĠŦŤĠĀĀŤTĀĀŤĠĠĀ 1157
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1038 GTTÁTTGTAGGAACGTTTCGGGATÁGGAÁTGTTTÁTTTGTGTÁACGAÁTTTTGÁTTTTŤ 1097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     919 GCGTŤITGAGTTTTAŤŤTŤTTŤTTAAGATTŤTTTAATŤTTTAGGTTGAATŤATAGTAG 978
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CC can be used in disgnostics and research, such as for treatment and disorders, industries of colon cancer antigens, given table, cardioactive, muscular; can be used in gene therapy. The colon cancer antigens can have cytostatic, cardioactive, muscular; colon cancer antigens can have cytostatic, cardioactive, muscular; colon cancer antigen polymuclectides, and can be used in gene therapy. The colon cancer antigen polymuclectides, and can be used antibodies to the proteins are useful for the prevention, colon cancer antigen polymuclectides, and cancer antigen polymuclectides, and colon cancer antigen polymuclectides, colon cancer. The colon cancer and cancer. The proteins and chisquosis of colon disorders, such as colon cancer. The colon cancer and cancer colon cancer and cancer colon cancer. The proteins colon cancer and disorders, muscular disorders, neural disorders, immune colon cancer disorders, reproductive disorders, infectious gystem disorders, muscular disorders, ancounted infectious and cardiovascular disorders. AAC98764 to AAC98772 and cancer cancer and cardiovascular disorders. AAC98764 to AAC98772 and cancer and cardiovascular disorders. AAC98764 to AAC98772 and cancer and cardiovascular disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulner immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon cancer antigen nucleotide sequence SEQ ID NO:187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; 85.
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                                                                                                                                                                                                                                                               Matches 294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon cantigens, useful for the treatment, prevention, and diagnosis of colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 610-611; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC97991 to AAC98763 encode the human colon cancer associated proteins,
                                                                                                                                                                                                                                                                                                                                                        Sequence 859 BP; 214 A; 219 C; 227 G; 193 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-587534/55.
                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                            1954 CTTCCCATCCTCACCACCGGGGCTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAG 2013
                                      2074 GGCTGGAGGCTCAGGGGCACTGGCACGGAACACCCTGAGGCCAGCCCTGGCTGC 2133
                                                                                                                                  2014 TGAÇAÇAÇAÇGTETÇAAAGAÇGÇTTÇTGGGGAATGAĞTGAĞÇGAAĞÇÇGTTTAÇGAĞTĞAÇTT 2073
     139
                                                                                      79 TGÁCÁCÁCÁGGTGTTCAÁÁGÁCGCTTCTGGGGÁGTGÁGGGÁÁGCGGTTTACGÁGTGÁCTT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
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                                                                                                                                                                                                                                                                                                Similarity
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gerregadertrones are area de la compara de l
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                                                                                                                                                                                                                                                                                                               96.4%;
                                                                                                                                                                                                                                                                                                          8.9%; Score 287.4; DB 21; Length 859; 96.4%; pred. No. 1.3e-67;
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                                                                                                                                                                                                                                                                                           Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary;
                                                                                                                                                                                                                                                                                                                         Gaps
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AAZ88700
ID AAZ8
XX
AC AAZ8
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AAZ88700 standard; DNA; 266 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer chemotherapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE19847779-C1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2194 AGCTCTTTCACTTCGGAGGATTGCTCAACAACCATGCTGGGCATCTGGACCCTCCTACCT 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krammer P, Mueller-Schilling M, Oren M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances a potentially useful for cancer chemotherapy. This sequence represents a potentially useful for cancer chemotherapy. Which contains a p53 binding fragment of the human CD95 receptor intron 1 which contains a p53 binding region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-162245/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2254 ÇTGGT 2258
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                                                                                                                                                                                                                                                                                                                                                                                                  Seguence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                           2500 GATCCCGCTGGGCAGGCGGGGGAGCTCCTCGGAAGACCACTGCGCGCTCCACGTT
                                      2560 GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGGAAGCTTTAGGGTCGC 2619
8.2%;
Similarity 99.2%;
                                                                                                                                         98DE-1047779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /bound_moiety= p53
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                                                                                                                                                                                                                                                                                                                                     Score 262.8; DB 2
Pred. No. 3.2e-61;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 266;
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Query Match
Best Local Similarity 100.0%; Proceeds to Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes human Fas (Apo-1). The specification describes antisense compounds which are targeted to the 5'-untranslated or 3'-untranslated region of start site, translational termination region of nucleic acid molecules encoding Fas, Fas associated protein 1, protein tyrosine expression of Fas, Fast or Fas associated protein 1, protein tyrosine expression of Fas, Fast or Fast in cells or tissues. They are used to treat autoimmune or inflammatory diseases such as hepatitis. They cannot not protein treat cancer, especially colon, liver or lumphoma
                                              Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
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                                                                                                                                                                                         Example 2; Page 71-73; 116pp; English.
                                                                                                                                                                                                           Antisense oligonucleotides for treating hepatitis and colon, liver or lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
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                                                                                                                                                                                                                                                                                                                 (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                           12-APR-1999;
                                                                                                                                                                                                                                                                                                                                                       10-APR-2000; 2000WO-US09540.
                                                                                                                                                                                                                                                                                                                                                                                                       WO200061150-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis; Fas associated protein 1; protein tyrosine phosphatase; cancer; autoimmune disease; inflammatory disease; lymphoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a human Fas (Apo-1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC61798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC61798 standard; DNA; 2551 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2620 TGGAGGGGGACCCCGGTTGGAGAGAGGAGGGGGAACTCCTGGACAAGCCCTGACAAGCCAA 2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marcusson EG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                      99US-0290640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Fag"
           7.8%; Score 252; DB 21; Length 2551; 100.0%; Pred. No. 1.2e-57; 7-2-1
     Indels
0; Gaps
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CC The present invention describes a polynucleotide library (I) useful in CC the molecular characterisation of a carrainoma, comprising a pool of CC polynucleotides or its subsequences which are either underexpressed in tumour cells, and correspond to any of the CC polynucleotide sequences chosen from the 468 sequences given in AB994010 (CC to AB94477. Also described: (I) a polynucleotide expressed or the prognosis or diagnostic of tumour, comprising (I) useful for CC (MI) differentially expressed polynucleotide sequences which are correlated with a cancer, involves obtaining a polynucleotide sample from CC a patient, and reacting the polynucleotide sample obtained with a probe CC of the polynucleotide sequences of (I), and cleating the polynucleotide sample obtained with a probe CC of the polynucleotide sequences of (I), and detecting the problemation of the problematic activities and can be used as anti-tumour senonded consisted in molecular characterisation of a carcinoma. (I) and (II) are
                                              RESULT 8
ABV94152
ID ABV9
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                                                                                                                                                                                                                                                      Claim 1; Page 206-207; 401pp; English.
                                                                                                                                                                                                                                                                               Novel polynucleotide library useful in molecular characterization of a carcinoma, comprising a pool of polynucleotide sequences or its subsequences which are either underexpressed or overexpressed in tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-619023/66.
                                                                                                                                                                                                                                                                                                                                                                               Bertucci F, Houlgatte R, Birnbaum D, Nguyen C,
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07-DEC-2001; 2001US-0007926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-2001; 2001WO-IB02811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200246467-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breast carcinoma related nucleotide sequence SEQ ID NO:143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2067 GTGACTTGGCTGGAGCCTCAGGGGCGGGGCACTGGCCAGCAGCACACACCCTGAGGCCAGCCC 2126
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RESULT 9
ABN79588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN79588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABN79588 standard; DNA; 2551 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immunosuppressive; antiinflammatory; hepatotropic; cytostatic; vasotropic; hepatitis; cancer; allograft reje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Fas locus HSAPO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                          09-MAR-2001; 2001US-0802669.
                                                                                                                                                                                                                                                                                                                                   10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                     US2002004490-A1.
                                                                                                                                                                                            12-APR-1999; 99US-0290640.
18-SEP-2000; 2000US-0665615.
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     Dean NM,
                                                                                                                 (DEAN/) DEAN N M.
(MARC/) MARCUSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2127
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                                                              (ZHAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGGCACGGAACACACCCTGAGGCCAGCCC 120
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                                                                                                                    MARCUSSON E G.
                                                              ZHANG H.
           Marcusson EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Fas HSAPO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8%; Score 252; DB 24; Length 2551; 100.0%; Pred. No. 1.2e-57;
                 Wyatt J,
                             Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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CC antisense oligonucleotides were designed to trarget human Fas.

CC Oligonucleotides were synthesised as chimeric oligonucleotides.

CC oligonucleotides were synthesised as chimeric oligonucleotides.

CC and are useful for treating an animal having an autoimmune or configuration of the allograft rejection, or ischemia reperfusion associated configuration apoptosis, allograft rejection, or ischemia are prevented by CC with apoptosis, allograft with the antisense oligonucleotide. The CC contacting the allograft with the antisense oligonucleotides. The contacting the allograft with the antisense oligonucleotides are used in diagnostics, therapeutics, prophylaxis CC oligonucleotides are used in diagnostics, therapeutics prophylaxis research research purposes. The present nucleotide sequence is CC useful for research purposes. The present nucleotide sequence is
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Best Local S
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Novel antisense compound targeted to nucleic acid encoding Fas, Fas ligand or Fas associated protein-1 is useful for inhibiting expression of Fas, Fas ligand, or Fap-1 in cells or tissues, and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABP35562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related to human Fas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX10416 standard; DNA; 2551 BP.
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                                                                                                                                                                                                                                                                                                                        DNA encoding protein differentially regulated in prostate cancer #85.
                                                                                                                                                                                        molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring;
                                                                                                                                                                                                                        prostate cancer; gene expression; differential regulation;
molecular marker; drug target; cancer detection; cancer diagnosis;
                                   WO200281638-A2
                                                                                               Homo sapiens.
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100.0%; Pred. No. 1.2e-57;
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17-OCT-2002.

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The invention describes genes (I) which are differentially regulated in CC sample comprising prostate tissue, which involves determining the number of the number is indicative of the probability that the sample comprises content at a subject having a prostate differentially regulated in the sample, where content in a subject having a prostate cancer. (I) Is useful for assessing a therapeutic or preventive content and in the sample comprises of the probability that the sample comprises content and interventially regulated in the sample comprises of target genes which are differentially regulated in prostate cancer. (I) is also useful for identifying agents that modulate a biological cells, which involves contacting a polypeptide differentially regulated in prostate cancer. (C (I) is also useful for identifying agents that modulate a biological cells, which involves contacting a polypeptide differentially-regulated in prostate cancer the test agent under conditions effective for cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and conditions especially relating, assessing, monitoring, prognosticating, compression of the polypeptide, and conditions especially relating predisposition to diseases and conditions especially relating predisposition to diseases and concer, it is stage of development, the nature of genetic defect, etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. (C office overly (I) can also be used as target for therapy or drug useful in the polypeptide and thus conditions of specific binding partners of the polypeptide. (I) is conditional applications to treat prostate cancer. The canded office of the polypeptide and thus conditions and disease pathways and the delineation of conditions and disease pathways and the delineation of canded in prostate cancer. The pathways which are present conditions to the appressed in the capture of the pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 252;
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                                      2127 TGGCTGCCCAGGCGGAGCTGCCTCTTCTCCCGCGGGTTGGTGGACCCGCTCAGTACGGAG 2186
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                                                                                                                                                                                 2067 GTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGGCACGGGAACACCCCTGAGGCCAGCCC 2126
                                                                                                                                                                                                                                                                                                                            2007 GCAAGAGTGACACAGGTGTTCAAAGACGCTTCTGGGGGAGTGAGGGAAGCGGTTTACGA 2066
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06-APR-2001; 2001US-281732P.
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                                                                                                                                       61 GTGÁCTTGGCTGGAGGCTCAGGGGCGGGCACTGGCACGGAACACACCTGAGGCCAGCCC 120
redecrecceáda de circi de contra de 
                                                                                                                                                                                                                                                                                  GCĀĀĠĀĠŦĠĀĊĀĊĀĠĀĠŦĠŦŦĊĀĀĀĠĀĊĠĊŦŦĊŦĠĠĠĀĠŦĠĀĠĠĠĀĀĠĊĠĠŦŦŦĀĊĠĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 100.0%; Pred. No. 1.2
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Query Match 7.0%; Score 226; DB 25; Best Local Similarity 100.0%; Pred. No. 8.4e-51;

Length 1024;

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The present invention describes a method (MI) for determining a CC expression profile of one or more human toxic response genes to a cC expression profile of one or more human toxic response genes to a cC described: (1) an array comprising one or more polynuclectides selected to ABZ84764, or their fragments of at least 20 nucleotides selected tomologues; and (2) determining the expression profile of the gene putatively identified to be a cor a human subject to a exposing cells to a exposing cells to a exposure to a exposure of cells comparising; (a) exposing cells to an agent or industrial agent, and cexpression profile of the gene after exposure of cells comparising; (a) exposing cells to an agent or isolating the test gene comparing the test profile to the expression profile of a gene after comparing the test profile to the expression profile for a putatively identified to be a comparing the test profile to the expression profile of a gene after comparing the test profile to the expression profile of a gene with correct to a known toxic pharmaceutical or industrial agent, comparing the test profile to the expression profile of a gene with correct to a known toxic pharmaceutical or industrial agent, and comparing the test profile to the expression profile of a gene with correct to a known toxic pharmaceutical or industrial agent, and comparing the test profile to the expression profile of a gene with correct to a cellular, organ or system level. The arrays comprising the human correct compounds and chemicals.
                                                                                                                              Sequence 1024 BP; 308 A; 226 C; 256 G; 234 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 294; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fas-delta-TM cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fas-delta-TM; transmembrane deletion; apoptosis; antibody; adoptive immunotherapy; transgenic animal; ss.
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                                                                                                                                                                                                                                                                                   New nucleic acid encoding Pas protein without its trans-membrane region - and related vectors, transformed cells, transgenic animals, protein and antibodies, useful for control of Pas mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-1995.
                                            mRNA was obtd. from human lymphocytes and PCR was used to make cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane region) mRNA. The PCR product was ligated into pBluescript and the recombinant plasmid was used to transfect E. coli DH5-alpha cells. recombinant plasmid was used to transfect E. given in AAQ93879. insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879 (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-200120/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barr PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-NOV-1993;
                                                                                                                                                                                                                              Claim 3; Fig.3-1 to 3-4; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR76238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LXRB-) LXR BIOTECHNOLOGY INC.
Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2033 GACGCTTCTGGGGGAGGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX24878 standard; DNA; 2471 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fas receptor; Fas ligand; Fash; proinflammatory; immunosuppressive; graft versus host disease; autoimmune disease; psoriasis; rheumatoid arthritis; systemic lupus erythematosus; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-1999.
                                                                                                                          Inhibition of proinflammatory responses - using an agent which modulates FasL stimulation, used for treating graft versus host
                                                                                                                                                                                                                                                                                   Chen J, Nabel GJ;
This present sequence is a DNA clone encoding soluble Fas receptor
                                                   Disclosure; Fig 4B; 71pp; English.
                                                                                                                                                                                                                                     WPI; 1999-132243/11.
                                                                                                                                                                                                          P-PSDB; AAW98070.
                                                                                                                                                                                                                                                                                                                                       (UNMI ) UNIV MICHIGAN
                                                                                                       disease or autoimmune disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (see AAW98070). The invention provides a method for inhibiting a constitution of proinflammatory response in a cell mixture by administering an consuppressive agent which inhibits the proinflammatory activity of Fas ligand (Fast). In some embodiments, Fast is coadministered neutrophil cells. The method can be practised in vitro, ex vivo or concludes that inhibit endogenous fast include antisense conviction of transforming growth factor (TGP)-beta, the method can be practised in vitro, ex vivo or concludes that inhibit endogenous fast expression, soluble fast creeptors, ribozymes that inhibit the endogenous expression of conditions of transforming growth factor (TGP)-beta, the method can be used for treating diseases associated constitute fast signalling agents that such as constituted fast-mediated proinflammatory response, e.g. constitutes the invention also provides a method darchiritis and psoriasis. The invention also provides a method for identifying agents which conditions a fast, arimilarion of a proinflammatory response, e.g. conditions also provides a method for identifying agents which
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                                                                                                                                              conflict
                                                                                                                                                                                          mat_peptide
                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                          Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.
                                                                                                                                                                                                                                                                                                                                  Human cell surface antigen.
                                                                                                                                                                                                                           sig_peptide
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12-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ29959 standard; cDNA to mRNA; 2534 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modulate FasL stimulation of a proinflammatory response
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                                                                                                                                                 product= Fas_antigen
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100.0%; Pred. No. 1.5e-50; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
        Homo sapiens.
                       antibody production; diseases; treatment; prevention; ds.
                                                                     Plasmid pF58 contg. human Fas cDNA.
                                        Plasmid pF58; human Fas cDNA; soluble membrane protein;
                                                                                                    19-FEB-1996 (first entry)
                                                                                                                                                       AAQ95297 standard; cDNA; 2534 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding human cell surface antigen - used to clarify apoptosis mechanism of various types of cell, and to prepare monoclonal antibodies that react with tumour cells expressing Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR28084.
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Search completed: August 1, 2003, 13:55:11 Job time : 1079.81 secs
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Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP07115988-A.
                                                                                                                                                                                                                                                                                                                                                                preparation of soluble membrane proteins - for their use in antibody production for the treatment and prevention of related diseases
                                                                                                                                                                                                                                                                                       AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The plasmid was used in the construction of an expression vector for the prodn. of recombinant soluble membrane proteins. The proteins can be used in antibody prodn. for the treatment and prevention of can be used in antibody prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                               (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                            Example 1; Pages 15-17; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR78606.
                                                                                                                                                                                                                                                         Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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9 US-09-834-291-187

11 US-09-834-291-32

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TITLE OF INVENTION: p53 Binding Areas
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122.
FILE REFERENCE: 4121-122.
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 201-08-21
CURRENT FILING DATE: 199-10-18
PRIOR FILING DATE: 199-10-18
PRIOR FILING DATE: 199-10-16
PRIOR APPLICATION UNMBER: DE 198 47 779.1
PRIOR PILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR PILING DATE: 1998-10-16
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US-09-834-291-1
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Patent No. US20020042064A1
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
APPLICANT: Oren, Moshe
                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
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Best Local Similarity 100.
Matches 3212; Conservative
121 AAGGCAAAGAAGTTTGGGGAACAGTATATAATTACCCCAACCCTTTGACATTAGCATAC 180
                                                                                                        61 TTTCCCCAGAACACCAGCATTCATTACGTGTTCATTCAATAGATTCTTCAAAGGATTCCA 120
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100.0%; Pred. No. 0;
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Gaps

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241 CEMAGNETISTEGACTINAGETISTA	PAAGGGCCCTGAGAAGTTTTGG
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AGTAACCAGAATTT 240 AGTAACCAGAATTT 240 AGTAACCAGAATTT 240 AGTAACCAGAATTT 240 AGTAACCAGAATTT 240 AGTAACCAGAATTT 240 AGTATCCTATCTCCTT 300 AGGGGTATGCAGAAGA 360 CTTTTATTTGTAAAG 480 TTTTTATTTGTAAAG 480 TTTTTATTTGTAAAG 480 AAGTAAGGAAGATC 540 AAGTAAGGAAGATC 540 AAGTAAGGAAGATC 540 AAGTAAGGAAGATC 540 AAGTAAGGAAGATC 560 AAGTGAACTTTTC 720 AATGAACTTTTC 720 AATGAACTTTTC 720 AAATGAACTTTTC 720 AAATGAACTTTTC 720 AAATGAACTTTTC 720 AAATGAACTTTTC 720 AAATGAACTTTC 720 AAATGAACTTTTC 720 AAATGAACTTTTT 1080 AAAGGGTTAT 1080	ACT A COLOR
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US-09-834-291-4
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                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
APPLICANT: Oren, Moshe
                                                                                                                                                                           sequence 4, Application US/09834291
Patent No. US20020042064A1
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TITLE OF INVENTION: D53 Binding Areas
FILE REFERENCE: 4121-122
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER:
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PRIOR APPLICATION NUMBER: DE 198 47
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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Best Local Similarity
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TITLE OF ANCES: TSPH-545 FILE REFERENCES: US/05/802,669 CURRENT ALLING DATE: 2001.03-09 FRIOR PILLATION NUMBER: US 05/655,615 FRIOR PILLATION NUMBER: US 05/230,640 FRIOR PILLATION NUMB	RESULT 3 US-09-802-669-94 US-09-802-669-94 Sequence 94, Application US/09802669 Sequence 94, Application US/09802669 ; Sequence No. US20020004490A1 ; PATELOANT: Nicholas M. APPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G. APPLICANT: Wyatt, Jacqueline APPLICANT: Wyatt, Jacqueline APPLICANT: Zhang, Hong APPLICAN	Qy 3060 CCATGGTGATTTCTGCTTGGTCTCCTGGTGGGGTTGGTGGTACTCCACCGCACAG 3119 2668 CCATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCCACCGCACAG 2727  Qy 3120 AACCCGGGGCCTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCT 3179 Qy 3120 AACCCGGGGCCTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCT 2787 Db 2728 AACCCGGGGCCTATTATTGGCCAAGAAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCT 2787 Db 2728 CAGAAATGCCAGCTTGCAGATGGCTAATCAAAG 3212 Qy 3180 CAGAAATGCCAGCTTGCAGATGGCTAATCAAAG 2820 Db 2788 CAGAAATGCCAGCTTGCAGATGGCTAATCAAAG 2820
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24; Indels 394; Gaps

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Sequence 3, Application US/09834291
Patent No. US20020042064A1
GENURAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
FITLE OF INVENTION: p53 Binding Areas
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DS 198 47 779.1
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Datentr, US-23
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                                                                                                                                                                                                                                                      ; TYPE; DNA; Homo Sapiens US-09-834-291-3
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US-09-834-291-3
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SEQ ID NO 3
LENGTH: 2380
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	1527 TITTCATATGGTTAACTGTCCAILCCASTATCUTTTTTTTCATATGGTTAACTGTCCATGCCAGGAACGTCTGTGAGCCTCTCATGTTGCAGCCA 1140	

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2368 TCAAAG 2373	3207 TCAAAG 3212 	2308 ACTTGAGCAGCCTGTTTTGAAAAAACCCCCCCCCCCCCC	3147 ACTTGAGCAGCCTGTTTTGAAAAGUCC LOCUSTANIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	2248 CTGGGGTTGGTGGTACTUGTICUGTACTACTATACTATACTACTACTACTACTACTACTACTAC	3087 CTGGGGTTGGTGGTACTCCGTTCCCACCGCGACAAAAACCCGGCGCCTATTATTGGCCAAAAAA 2307	2188 CTTTCTTTTTGCCCTTTCTIAGCCACCCCCTATTATTGGCCAAGAA 3146	3027 CTTTCTTTTTGCCCTTTCTTAGCTTVGGACT-CCACCGTGATTTCTGCTTGGTCTCCTG 2247	2128 CTTTAAGACTGTAAGTCGCIGCCIGAGIGGATTGGTGATTTCTGCTTGGTCTCCTG 3086	2967 CTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTCATTAGTATGTTTTCTTGCCCTTCT 2187	2068 ACCGITITITATIGICACACACACACACACACACACACACACACACACACAC	2907 ACCGTTTTTATTGTCACACAGAAAAGGAAACTSCTTTTTCCTTCCGGGAATTCTCT 2127	2008 GCACCTTTTCTTTCTCUGAAAAAAGITATAAAAAAAAAAAAAAAAAAAAAAAAAAA	2847 GCACCTTTTCTTTCTGGAAAAGTTAIAIGGGGGTGAATGAGCTTCTGGAGGCTTGTTT 2067	1948 CAGACGTAGGAAATAAGICAGCTTCTTT 2906	2787 CAGACGTAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAAGGACTCGGAAGAACG 2007	1888 GGGGGCGGGAGAGAGCCCIGCAGCCCIA CARCATTA AGCCGGAAGGCTCGGAAGAACG 2846	2727 GGGGGGGGAGAGAGCCTACAGCCTICAGAACACATTTTCTGGCAGTTCT 1947	1828 CCTGACAAGCCAAAGCCAAAGGTCCGCTCCCCTCTTTTTCTGCAGCAGTTCT 2786	2667 CCTGACAAGCCAAAGCCAAAGGTCCGTCCGCCGCGCGCGC	1768 GCTTTAGGGTCGCTGGAGGGGAACCCCCGC 2726	2607 GCTTTAGGGTCGCTGGAGGGGGACCCCCGGTTGGAGAGGGGGAACTCCTGGACAAGC 2666

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US-09-834-291-2
US-09-834-291-2
; Sequence 2, Application US/09834291
; Sequence 2, Application US/09834291
; Sequence 2, Application US/09834291
; Sequence 2, Application US20020042064A1
; Patent No. US20020042064A1
; Patent No. US20020042064A1
; Patent Fillo Coren, Moshe Binding Areas
pricts OF INVENTION: p53 Binding Areas
pricts OF 11202
pricts Reprictation NUMBER: US/09/834,291
CURRENT APPLICATION NUMBER: PCT/DE99/03343
prior Application NUMBER: PCT/DE99/03343
prior Application NUMBER: DE 198 47 779.1
prior Application NUMBER: DE 198 47 779.1
prior Filling DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 720
TYPE: DNA
GRGANISM: Homo Sapiens
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22.2%; Score 713; DB 9; Length 720; Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-186; Best Local Similarity 100.0%; Mismatches 0; Indels
Matches 713; Conservative 0; Mismatches

0;

Gaps

0;

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GENERAL INFORMATION:

APPLICANT: ROSEN et al.

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

NUMBER OF SEQ ID NOS: 1556

SOFTMARE: Patentin Ver. 2.0

LENGTH. 626
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US-09-925-299-187
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Patent No. US20020055627A1
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FEATURE:
NAME/KEY: misc feature
LOCATION: (803)
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                                                                                  LENGTH: 859
TYPE; DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 ccerrictraderricaence arcesarder sarricte de ridere de cerce de deserradores 600
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FILE REFERENCE: PALOS

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: COT/US00/05883

PRIOR APPLICATION NUMBER: COT/US00/05883

PRIOR PILING DATE: 2000-03-08

PRIOR PILING DATE: 1909-03-12

VOUNBER OF SEQ ID NUMBER: 60/124,270

VOUNBER OF SEQ ID NOS: 1556

SOPTMARE: Patentin Ver. 2.0

LENGTH. 552
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APPLICANT: Rosen et
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NAME/KEY: misc_feature
LOCATION: (803)
OTHER INFORMATION: n equals a,t,g, or c
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                                                                                                                                                                                                                                                                                                                                                                                                     Match
8.9%; Score 287.4; DB 11; Length 859;
Local Similarity 96.4%; Pred. No. 1.7e-68;
es 294; Conservative 0; Mismatches 11; Indels 0;
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LOCATION: (853)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                      1954 CTTCCCATCCTCACCACCGGGGCTTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAG 2013
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2014 TGACACACAGGTGTTCAAAGACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTT 2073
                                                                                                                               2254 CTGGT 2258
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o. US20030040617A9
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; Pred. No. 1.7e-68;
0; Mismatches 11; Indels
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PACENTE PLICATION US/09834291

PACENT NO. US2002042064A1

PACENDEAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Waller-Schilling, Martina
APPLICANT: Oren, Moshe
FILE REFERENCE: 4121-122

FILE REFERENCE: 4121-122

CURRENT PAPLICATION NUMBER: US/09/834,291

CURRENT FILING DATE: 2001-08-21

CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: DE 198 47 779.1

PRIOR FILING DATE: 1998-10-16

PRIOR FILING DATE: 1998-10-16
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; ORGANISM: Homo Sapiens
US-09-834-291-32
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                               US-09-802-669-1
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SEQ ID NO 32
LENGTH: 266
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Sequence 1, Application US/09802669 Patent No. US20020004490A1
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Local Similarity 99.2%;
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                                                                                                                            2740 GAGCCTACAGCCTTCAGAACACATAT 2765
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APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
APPLICANT: Zhang, Hong
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE REFERENCE: ISPH-545
FILE REFERENCE: ISPH-545
CURRENT FILING DATE: 2001-03-09
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1009-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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                                                                                                                                US-09-949-713-16
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JOURNAL: J. Biol. Chem.
VOLUME: 267
Sequence 16, Application US/09949713
Patent No. US20020044944A1
GENERAL INFORMATION:
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LOCATION: (221)..(1228)
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PAGES: 10709-10715
DATE: 1992-05-25
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100.0%; Pred. No. 2.4e-58;
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APPLICANT: NAKANURA, NO. US20020044944A1io
APPLICANT: NAKANURA, Shigekazu
APPLICANT: NAKANURA, Shigekazu
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/949,713
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/09/180,100
PRIOR APPLICATION NUMBER: US/09/180,100
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25

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                                                                                                                                                                                                                                                                                      US-09-884-987-1
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                                                                                                                                                                                                                Matches 226;
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ś
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; ORGANISM: Homo sapiens
US-09-949-713-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09884987
Patent No. US20020102653A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
                                                                                                                                                                                                                                                                                            NAME/KEY: polyA site
LOCATION: (2352)...(2357)
NAME/KEY: polyA site
LOCATION: (2518)...(2532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAGATA, Shigekazu et al
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
FILE REFERENCE: 0020-4877P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: sig_peptide
LOCATION: (195)..(242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 16
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (195)..(1199)
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: mat peptide LOCATION: (243)..()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: polyA site LOCATION: (1831)..(18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                     Local
                                                   61 ddcachddcacddaacacachcachchchddchddchdchdchdchddddaadchdchdchriti 120
2153 CTCCCGCGGGTTGGTGGACCCCGCTCAGTACGGAGTTGGGGAAGCTCTTTCACTTCGGAGG 2212
                                                                              2093 GGCACTGGCACGGAACACCCCTGAGGCCCAGGCCCTGGCTGCCCAGGCGGAGCTGCCTCTT 2152
                                                                                                                                                2033 GACGCTTCTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCG 2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2213 ATTGCTCAACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGT 2258
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                                                                                                                          1 GACGETTETGGGGAĞTGAĞĞĞAAĞEĞĞTTTACĞAĞTĞAETTĞĞETĞĞAĞEETEAĞĞĞĞĞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CTCCCGCGCGCTTGGACCCGCTCAGTACGGAGTTGGGGAAAGCTCTTTCACTTCGGAGG 180
                                                                                                                                                                                          h 7.0%; Score 226; DB 10; Lengun 2. Similarity 100.0%; Pred. No. 3.7e-51; 0: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GGCACTGGCACGGAACACACCCTGAGGCCAGGCCTGGCTGCCCAGGCGGAGCTGCCTCTT 120
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                                                                                                                                                                                                                                 DB 10; Length 2534;
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RESULT 13
US-09-736-457-796/c
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PRIOR APPLICATION NUMBER: US/02/04-30

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1909-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PILING DATE: 1999-08-09

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PRIOR SEQ ID NOS: 325720

SOPTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
IITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
IITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C1.5
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 796,
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 816
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                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 AÁGÁTAGTÁCÁGÁAÁAÍTTCCCÁCÁTACTGCACACCGTTTCCCCCTGTTTTTAACATTTTÁT 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757 GAGATAATACAGAGAATGCCCATATACCATCCTCCTTATCCCACTTCTTTTTGTGTCTAT 816
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US20020168637A1
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                                                                                                                                                                                       Carter, Darrick
Retter, Marc
Mannion, Jane
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Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                                                                                                                                                                                            Vedvick,
                                                                                                                                                                                                                                                                                   Fanger, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.9%; Score 60.8; DB 13; Length 816; Conservative 0; Mismarch-
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-736-457-796
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APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Hangur, Chaitanya S.
APPLICANT: Hangur, Chaitanya S.
APPLICANT: HONABD, Andria
APPLICANT: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION NUMBER: US/09/902,941
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2001-07-10
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US-09-902-941-796/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: APPLICANT: Retter, Marc
APPLICANT: Carter, Marrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 796
LENGTH: 2435
TYPE: DNA
ORGANISM: Homo sapiens
US-09-902-941-796
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                                                                                                            Sequence 796, Application US/09849626 Publication No. US20020197669A1 GENERAL INFORMATION:
             APPLICANT: Bangur, Chaitanya
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: Switzer, Anne
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2374 TAGATTTACAGAGAAGTTGCÁGAGATAGTACAAAGAGTTCCTGTATACACCTTCACC 2319
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      Switzer, Anne
McNeill, Patricia
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LENGTH: 2435
TYPE: DNA
ORGANISM: Homo sapiens
US-09-849-626-796
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Search completed: August 1, 2003, 13:36:32
Job time : 846.884 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE REFERENCE: 210121.478C16
CURRENT PRILING DATE: US/09/849,626
CURRENT FILING DATE: 2001-05-03
CURRENT FILING DATE: 2001-05-03
CURRENT FILING DATE: 1026
CURRENT FILING DATE: 1026
CURRENT FILING DATE: 1026
                                                                                                                                                                                                                                                                  1.9%; Score 60; DB 10; Length 2435; Query Match
Best Local Similarity 69.8%; Pred. No. 2.8e-05; Indels 0 Matches 81; Conservative 0; Mismatches 35; Indels 0
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                                                                                              2374 TAGATTTACAGAGAAGTTGCAGAGATAGTACAAAGAGTTCCTGTATACCCTTCACC 2319
                                                                                                                                                                                                                            676 TITTCCTTCCTTCTTTTACATTTTTTTTTTAAATGAACTTTTCATTTTGGAATAGTTT 735
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## us-09-834-291-6.rge

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OM nucleic - nucleic search, using sw model
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Perfect score:
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Maximum DB seg length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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RESULT AX02609 LOCUS DEFINIT ACCESSI VERSION KEYWORK SOURCE ORGAN REFERE AUTH	CCC	
RESULT 1 LACUS 1094 LOCUS DEFINITION ACCESSION VERSION	Orre 188.4 1	
TH. PPSP	92.00 92.00	
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                     Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 1984779-C 7 03-FEB-2000;
DEUTSCHES_KREBSFORSCH (DE)
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                         Homo sapiens
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent, DE 19847779-C 5 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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DEUTSCHES KREBSFORSCH (DE)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol type="genomic DNA"
/db_xref="taxon:9606"
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                                                    Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
Substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 24 03-FEB-2000;
                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                               Homo sapiens
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Novel receptor dna useful for identifying apoptosis-modulating
Bubstances potentially useful for cancer chemotherapy
DEUTSCHES KREBSFORSCH (DE)
DEUTSCHES KREBSFORSCH (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/mol type="genomic DNA"
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/mol_type="genomic DNA"
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Local Similarity 95.0%;
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Sequence 32 from Patent DE19847779.
AX026120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                              Mueller,M., Wilder,S., Bannasch,D., Israeli,D., Lehlbach,K., Li-Weber,M., Friedman,S.L., Galle,P.R., Stremmel,W., Oren,M. and Krammer,P.H.
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AJ011034.1 GI:4165483
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                              CD95 gene; enhancer.
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                                                       GERMANY
                                                                  Submitted (08-SEP-1998) Mueller M., Department of Internal Medicine IV, University Hospital, Bergheimerstr. 58, Heidelberg, 69115,
                                                                                                Direct Submission
                                                                                                                 Mueller,M.
                                                                                                                                                                    p53 activates the CD95 (APO-1/Fas) gene in response to DNA damage
by anticancer drugs
J. Exp. Med. 188 (11), 2033-2045 (1998)
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|mol_type="genomic DNA"
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Pred. No. 4.2e+02;
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160 GGACAAGCCCTGACAAGCCA 179
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 2 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 3 from Patent DE19847779.
AX026091
                                                                         Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 3 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)
                                                                                                                                                                                                                              Homo sapiens
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Similarity 95.0%;
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                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                Homo sapiens (human)
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159. .178
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159. .178
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
181 c 216 g 18:
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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Pred. No. 2.4e+02;
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                                                                                                                           Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 1 03-FEB-2000;
DEUTSCHES_KREBSFORSCH_(DE)
                                                                                                                                                                                                                                                                                                                            AX026089 3212 bp
Sequence 1 from Patent DE19847779.
AX026089
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy patent: DE 19847779-C 4 03-FEB-2000; DEUTSCHES_KREBSFORSCH (DE)
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Sequence 4 from Patent DE19847779.
AX026092
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Similarity 95.0%;
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                                                                                                                      Location/Qualifiers
                                                   /db_xref="taxon:9606"
784 c 809 q
                                                                           organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/db_676 c 657 g 76
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595 c 568 g
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 DB 6;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
             requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
one plasmid subclone or more than one M13 subclone; and the
assembly was another and by activations were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10653 GGACAAGCCCTGACAAGCCA 10672
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assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                        Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                               Blakey, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAAAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL157394.15 GI:15384622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete sequence.
AL157394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 03008583-A 1262 30-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morris,D.W. and Engelhard, E.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX695635.1 GI:29418787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1262 from Patent WO03008583. AX695635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (human)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
&836 c 9010 g 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.0%; Score 18.4; DB 6; Length 45121; 95.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.0%;
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om clone RP11-399019
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FEATURES
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AC139121
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                                                   REFERENCE
AUTHORS
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VERSION
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Best Local Similarity
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                                                                                                             JOURNAL
                                                                                                                                         TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The true right end of clone RP11-304T5 is at 18704 in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/HGP/Chr10
RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGAAAAGCCCTGACAAGCCA 20
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                                                                                                                                                              Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M. F., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A., and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS PHASE2; HTGS DRAFT.
Didelphis virginiana (North American opossum)
Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Didelphis virginiana clone LB3-39J13, WORKING DRAFT SEQUENCE, 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Metatheria, Didelphimorphia, Didelphidae, Didelphis. 1 (bases 1 to 167075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC139121
Submitted (24-JAN-2003) NIH Intramural Sequencing Center, 8717
                                                                                                                                                                                                                                                                                                                                                                                                                               Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
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                                                      Green, E.D.
                                                                                                                                         NISC Comparative Sequencing Initiative
                              Direct Submission
                                                                               (bases 1 to 167075)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Sequence from AC015461 sequenced by WIBR."
105973. 105989
/note="Sequence confirmed by AC015461 sequenced by WIBR."
a 36398 c 36888 g 58358 t
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100119. .100156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Sequence from AC015461 sequenced by WIBR." 105808. .105972
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100157. .100198
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
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    Mismatches

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Pred. No. 1e+02;
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COMMENT
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                               misc_feature
                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * the accession number will be preserved.
1 117048: gap of 117048 bp in length
1 117049 117148: gap of unknown length
1 117149 119135: contig of 1987 bp in length
1 119136 119235: gap of unknown length
1 119136 119235: gap of unknown length
1 119136 119259: gap of unknown length
1 119136 119159: gap of unknown length
1 119149 119149: contig of 7788 bp in length
1 140948 141047: gap of unknown length
1 141048 167075: contig of 26028 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 167075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 166581 bases at least Q40
Consensus quality: 166589 bases at least Q30
Consensus quality: 166648 bases at least Q20
Insert size: 156075; sum-of-contigs
Quality coverage: 10.81x in Q20 bases; sum-of-contigs
Quality coverage: 9.73x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: 039J13
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                                   /note="assembly_fragment"
119236. .133059
                                                                                                         vector side:left"
117149. .119135
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                                                                                                                                                                                                                                                                                                                                /organism="Didelphis virginiana"
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1. .117048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                           /clone="LB3-39J13"
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         18;
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                                                                                                                                                                                                                                                                                                                                             WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated
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     h 87.0%;
Similarity 94.7%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
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Made, C. M., Kulbokas, E. J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.

The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STS size: 714
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Tel: 6172521477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
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$212P00375FC6.TO CZECHII/Ei Mus musculus STS genomic, sequence
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                                                                                                                                                                                         /organism="Mus musculus"
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                                                                                                                    /db xref="taxon:10090"
/map="+ 16 22-505 92651644-92652127"
/clone 11b="CZECHII/Ei"
<1. .>714
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 Score 17.4; DB 11;
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Oy 2 GAAAAGCCCTGACAAGCCA 20
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Search completed: August 1, 2003, 17:32:44 Job time: 81.1573 secs

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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                                                  Score
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7098.748 Million cell updates/sec
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603049567F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189752 5',
                          Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can l

Clone distribution: MGC clone distribution information can l

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

http://image.llnl.gov

plate: LLAM11474 row: e column: 17
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                              BI763679.1 GI:15755257
                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                     mRNA sequence.
                 High quality sequence stop:
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T79683 yd7lc09.rl
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AZ630360 1M0483H23

BQ0362540 RC0--ST018

B1924611 EST594500

BH027622 RPCI-24-3

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AA625121 af67d12.r

BE353461 EST35383

BW473986 BW470998

BY470998 BY470998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgi-bin/cluster.cgi?seq=CSDDE002DG09QP1&cluster=5554.r. Contact Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODE002DG09QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 GGACAAGCCCTGACAAGCCA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5554.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Feb 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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5-PRIME, mRNA sequence.
AL540709
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/clone_lib="NIH_MGC_116"
/note="Organ: pooled_colon, kidney, stomach, Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
stomachs, 62 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
insert size range 1-3 kb. Library is normalized and
scruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
/CLOUDE CONTROLL CONT
                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="CS0DE002YN18"
                                                                                                                                                                                                                                                                                                                                                                           /organism≈"Homo sapiens"
/mol_type≈"mRNA"
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/mol_type="mRNA"
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one="IMAGE:5189752"
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RESULT 4
BQ091744
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BQ072834
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                                                                                                                    369 GGACAAGCCCTGACAAGCCA 388
BQ091744 255 bp mRNA linear EST 08-APR-200
UMN21B02 Canine Brain cDNA Library Canis familiaris cDNA 5', mRNA
                                                                                                                                                      1 GGAAAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12796 row: l column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1089)
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                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_118"
/clone_lib="NIH_MGC_118"
/note="Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
cloning). Average insert size 1.7 kb, insert size range
cloning). Average insert size 1.7 kb, insert size range
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
180 a 263 c 333 g 212 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5756324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://mgc.nci.nih.gov/.
Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 26
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                   EST 08-APR-2002
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BQ091744
BQ091744.1 GI:20071739
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 255)
Roberts, M.C., Hendrickson, J.A., Hoffmann, D.E., Plickinger, G.H., Rutherford, M.S., and Mickelson, J.R.
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Contact: Mickelson, J.R.
Veterinary PathoBiology
Veterinary PathoBiology
University of Minnesota
1988 Fitch Avenue, University of Minnesota, St. Paul, MN 55108, USA
1988 Fitch Avenue, University of Minnesota, St. Paul, MN 55108, USA
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BIT84680 sef57h10.y3 Gm-c1078 Glycine max cDNA clone GENOME SYSTEMS CLONE
BAF57h10.y3 Gm-c1078 Similar to SW:SUI1_ORYSA P31278 PROTEIN
ID: Gm-c1078-380 5' similar to SW:SUI1_ORYSA P31278 PROTEIN
TRANSLATION PACTOR SUI1 HOMOLOG ;, mRNA sequence.
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                                                                                                                                                                                                                                                                   Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna Shoemaker, R., Keim, P., Vodkin, L., Enpelding, J., Martin, J., Beck, C., R., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Boek, G., Bolla, B., Materwood, K., Steptoe, M., Theising, B., Allen, M., Schurk Wylie, T., Underwood, K., Steptoe, M., Pape, D., Harvey, N., Schurk Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann Y., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST project
Public Soybean EST project
Public Soybean EST project
Washington University School of Medicine
Washington University School of
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public Soybean EST project
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/db_xref="taxon:9615"
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94.7%;
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pred. No. 3.8e+02;
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BE272685
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                                                                         VERSION
                                                                                                                                       ACCESSION
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Email: est@watson.wustl.edu

Trace considered overall poor quality This clone is available

Trace considered overall poor Corp. 2130 South Memorial Parkway

through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway

Huntsville, AL 35801 For further information call: (800)-533-4363

Huntsville, AL 35801 For further commact via email: ccu@resgen.com

or contact via email: ccu@resgen.com
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High quality sequence stop: 1.
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          Homo sapiens (human)
                                                                                                   BE272685.1 GI:9147035
                                                                                                                                                                                                      mRNA sequence.
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/clone="genome systems of 7 day old 'Bragg' supernodulating
/tissue type="Roots of 7 day old 'Bragg' supernodulating
mutant NTS382 seedlings"
mutant NTS382 seedlings"
/dev Etage="7 days old"
//tissue-roots
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xref="taxon:3847"
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94.7%;
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Pred. No. 4.1e+02;
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cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium (LLNL) found through the I.M.A.G.E. Consortium information can be Plate: LLCM202 row: k column: 18 Consortium/LLNL at: image.llnl.gov High quality sequence stop: 536.
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                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556 GAAAAGCCCTGTCAAGCCA 574
                                                                                                                                                                                            NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (Dases 1 to 813) (Chases 1 to 813)
                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                        601174770F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3530249 5',
                                                                                                                                                                                                                                                                                                                                                                          BE296494.1 GI:9180056
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High quality sequence stop: 609.
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="PH10B (phage-resistant)"
/clone lib="NH MGC 14"
/clone lib="NH MGC 14"
/note="POTGAIN: Kidney, Vector: POTB7; Site 1: XhoI; Site 2: ECORI, CDNA made by oligo-dr priming. Directionally cloned into ECORI/KhoI sites using the following 5; lasert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Gerald M. Rubin (University of Gerald M. Size-Selected Souph Hong in (Stratagene) and Superscript II RT (Life Technologies)."
137 c 212 g 147 t
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/clone="IMAGE:3347822"
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/mol_type="mRNA"
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BQ070571
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                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: Plate: LLCM2090 row: 1 column: 12
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; (bases 1 to 1062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
/clone="IMAGE:592271"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH10B (phage-resistant)"
/clone_lib="NH1 MGC 47"
/clone_lib="NH1 MGC 47"
EcoRI, cDNA made by oligo-dT priming. DIrectionally cloned into EcoRI/KhoI sites using the following 5/
insert size 1.8kb. Library constructed by Ling Hong in (Stratagene) and Superscript II RT (University of (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGENCOURT_6839245 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5922971
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                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://mgc.ngi.nih.gov/.
1 Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                  sequence stop: 624.
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/mol type="mRNA"
/db_xref="taxon:9606"
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/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_17"
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94.7%;
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BASE COUNT ORIGIN

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                                                                                                  Local Similarity
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Hillier, L., Clark, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
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Location/Qualifiers
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Insert Size: 1976
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                                                                      18; Conservative
       1 GGAAAAGCCCTGACAAGCCA 20
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                                                                                                                                                                                                                             /dev stage="20 week-post conception fetus"
/dev stage="20 week-post conception fetus"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Soares fetal liver spleen lNFLS"
/note="Organ: Liver and Spleen; Vector: p7773D (Pharmacia)
/with a modified polylinker; Site_1: Pac I; Site 2: Eco RI;
with a modified polylinker; Site_1: Pac I; Site 3: Eco RI;
/strand cDNA was primed with a Pac I adaptors
/double-stranded cDNA was ligated to Eco RI adaptors
/double-stranded cDNA was ligated to Eco RI
/for RI;
//double-stranded cDNA was ligated to Eco RI
/double-stranded cDNA was ligated to Eco 
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/db xref="taxon:9606"
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100.0%; Pred. No.
tive 0; Mismatc
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FOCAS
                         BZ764825/c
                                                             RESULT 11
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Hultman, M., Kucaba, T., Le, M., Tan, F., Trevaskis, E., Waterston Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                 179 GCAAAGGCCCTGACAAGCCA 198
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stops: 244 Source: IMAGE Consortium, LINL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1814 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 1814
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_ESTs: yd71c09.sl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13RP1
                                                                                                                                                                                                                 1 GGAAAAGCCCTGACAAGCCA 20
      BZ764825
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             105 a
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   /den stage="20 week-post conception fetus"
//lab host="DH10B (ampicillin resistant)"
//lab host="DH10B (ampicillin resistant)"
//lab host="DH10B (ampicillin resistant)"
//lab host="DH10B (ampicillin resistant)"
//lab host="DH10B (ampicillin resistant)
//lab host="DH10B (ampicillin resistant)
//lab host="DH10B (ampicillin resistant)
//lab host="DH10B (pharmacia)
//lab "Strand plus primed with a Pac I - oligo [dT] primer
ist strand cDNA was primed with a Pac I - oligo [dT] primer
ist strand cDNA was ligated to Eco RI adaptors
double-stranded cDNA was ligated to Eco RI adaptors
constructed by Bento Soares and M.Fatima Bonaldo."

constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L. .389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GDB:469297"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                            90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type="mRNA
                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                            Score 16.8; DB 14;
pred. No. 8.9e+02;
                   421 bp
                         DNA
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                      Length 389;
                             linear
                             GSS 13-MAR-2003
                                                                                                                                                                                                                                                                                                  0;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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                                      JOURNAL,
                                                                                                                                              AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 GAÁAÁÁGCCCTGAAÁAGCCA 376
                             Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                          AA233020
AA23020
AA2308.r1 Soares NhHWPu S1 Homo sapiens cDNA clone IMAGE:666422 5' similar to gb:M55905 MALATE OXIDOREDUCTASE (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGAAAAGCCCTGACAAGCCA 20
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                         AA233020.1 GI:1856013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 421)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Ga,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At4g2410 Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SALK_127083.30.15.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_127083.30.15.n, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                               sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Clone="SAIK 127083.30.15.n"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 77 c 87 g 144 t
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/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an annotated intron of At4g24160.
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                                                                                                                                                                                                                                                                                                                                     EST 06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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            FEATURES
                                                                                                                                                                   COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GCAAAGGCCCTGACAAGCCA 320
                                  http://genome.arizona.edu/orders/
                       Seq primer: T3
                                                                                                                                                             Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                          Solanum tuberosum (potato)
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGAAAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                      BM109280.1 GI:17070044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 a
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5428454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGE:666422"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Email: potato-array@tigr.org
This clone can be obtained from the Univer
Institute. Orders can be made through URL:
                                                                                                                                                                                                               van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S., Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
Generation of ESTs from potato roots
                                                                                         The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (Dases 1 to 434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM109280 434 bp mRNA linear EST 10-MAR-:
EST556816 potato roots Solanum tuberosum cDNA clone cPRO3B10 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1352 Std Error: 0.00

Seg primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clome lib="Soares NhHMPu S1"
/Clome lib="Soares NhHMPu S1"
/Dote="Urgan: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
whHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Pollowing HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab host="UH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%; Score 16.8; DB 9; Length 426; 90.0%; Pred. No. 9.2e+02;
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                        from the University of Arizona Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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CPRO3B10 5' end
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                                                                                                                                                                                                                                                                                                                                                                                                                  source
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AGENCOURT 10616779 NIH MGC_169 Mus musculus cDNA clone
IMAGE:6743287 5', mRNA sequence.
BU962533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 440)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU962533.1 GI:24192105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: LLCM3082 row: 1 column: 06 High quality sequence stop: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Michael Brownstein Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Jonathan Kuo, NIMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAAAGCCGAGACAAGCCA 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

98 c 82 g 129 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="roots"
/dev stage="in vitro grown stem cuttings"
/lab_host="SOLR"
                                                                                                                                                   /lab host="DH10B (T1-phage-resistant)"
/clone lib="NIH MGC 169"
/note="Organ: Testicles; Vector: pDNR-LIB; Site 1: SfiI
/ggcgattatggcc); Site 2: SfiI (ggcggcctggcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4113"
/clone="cPRO3B10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Solanum tuberosum"
5'-AAGCAGTGGTATCAACGCCAGAGTGGCCATTACCGCCCGGG-3' and 5'-AATTCTAGAGCCGAGGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5 kb size fraction. Library created in thelaboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib="potato roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6743287"
                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%;
90.0%;
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Pred. No. 9.2e+02;
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                                                                                                                                  Matches
                                                                                                                                                                                          Query Match
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433 GGCÄÄÄGCCCTCÄCÄÄGCCA 414
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7e84d08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3289167 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE646301.1 GI:9970612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    info@image.llnl.gov
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                 1 GGAAAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAAAGGCCCTGACAAGCCA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 450)
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                                                                                                                                                                                                                                                                                                 87
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                       /lab_host="DHIOB"
//lab_host="DHIOB"
//clone lib="NCI CGAP Pr28"
//clone lib="NCI CGAP Pr28"
//note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
/note="Organ: prostate; Vector: p1773D-Pac (Pharmacia)
/note="Organ: prostate; Vector: p1873d-Pac (Pharmacia)
/note="Organ: prostate; Vector: p1873d-Pac (Pharmacia)
//note="Organ: p1873d-
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Pred. No. 9.3e+02;
                                                                                                                                                                     Score 16.8; DB 10 Pred. No. 9.4e+02
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                                                                                                                                      Mismatches
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                                                                                                                                                                                                DB 10;
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                                                                                                                                                                                                    Length 450;
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Search completed: August Job time: 72.4754 secs

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CDNA encoding huma

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Human

colon tumour tumour

Human oestrogen re Human oestrogen re Human lung specifi Partial nucleotide

Gene encoding huma

Human ovarian and propionibacterium Human immune/haema

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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                 pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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22: /SIDS1/gcgdata/genesed/geneseqn-emb1/NA2000.DAT:*
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                                                                                                                AAZ88700
AAF64773
ABZ19870
                                                                                              AAS40992
                  ABL89871
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8059.612 Million cell updates/sec
                                                                                                         Human CD95 recepto
Novel human polynu
Group III cDNA can
cDNA encoding nove
                                                                                                                                                                                                               Description
                                                                  Sequence encoding Mitochondrial NAD
                           Human polynucleoti
                                                  Thyroid cancer rel
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RESULT 1
AAZ88700
ID AAZ8
XX AAZ8
XX AAZ8
XX II-M
DT 11-M
XX P53;
XW Canc.
XX Canc.
XX Homo
XX Key
FT Prot-
FT 
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                                                                                                                                                                                                                                                                                                                                                      p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                                                                                                                                                         Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                        cancer chemotherapy; 88.
                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                             DE19847779-C1.
                                                                                                                                            03-FEB-2000.
 Krammer P, Mueller-Schilling M, Oren M;
                                                                        16-OCT-1998;
                                                                                                           16-OCT-1998;
                                   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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                                                                              98DE-1047779.
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                                                                                                                 98DE-1047779.
                                                                                                                                                                                                                                                          Location/Qualifiers 160..179
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/bound_moiety= p53
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AAF44731
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AAT36899
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Secreted protein-e
Receptor #71 parti
Human ORFX polynuc
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Human prostate exp
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Human nervous syst
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The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 620; 1046pp; English.
                                                                                                                                  Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                               Williams LT, Escobedo J, Innis MA, Garcia PD, Klin
Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson
Crkenjakov R, Drmanac S, Dickson M, Labat I, Leshk
Kita D, Garcia V, Jones LW, Strache-Crain B;
                                                                                                                                                                                                       WPI; 2001-091805/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                        02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                  02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000WO-US18374.
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200102568-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polynucleotide, SEQ ID NO: 529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF64773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF64773 standard; cDNA; 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 binding region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 4; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 GGACAAGCCTGACAAGCCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; gene therapy; colon cancer; prostate cancer;
                                                                                                                                                                                                                                                                                               HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                              99US-0142310.
                                                                                                                                                                                                                                                                                                                                 99US-0142311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.0%; Score 18.4;
95.0%; Pred. No. 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                                                                                                                              Leshkowitiz D;
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                                                                                                                                                                                                                                    Klinger J, Kassam A;
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RESULT 3
                                          ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and invention. (I) and (II) have cytostatic activity and can be used in gene present prosent invention are useful for diagnosing, preventing and treating immune response. They can also be useful in virology, microbiology, molecular biology and recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
       at ftp.wipo.int/pub/published_pct_sequences.
                                 specification,
                                                                                                                                                                               Claim 1; SEQ ID 2296; 207pp; English.
                                                                                                                                                                                                                       New immunogenic polynucleotides or polypeptides useful for diagnosing, preventing and treating cancer expressing CT or CP mRNA antigens, and
                                                                                                                                                                                                              in virology, immunology, mirecombinant DNA techniques
                                                                                                                                                                                                                                                                                  WPI; 2003-058387/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                            09-JAN-2002; 2002US-347313P
                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001US-280255P.
28-AUG-2001; 2001US-315563P.
                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2002; 2002WO-US10421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200278516-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response; virology; immunology; recombinant DNA technology; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group III cDNA cancer related clone SEQ ID NO:2296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ19870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ19870 standard; cDNA; 502 BP
          The sequence data for this patent did not form part of the printed ification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and treat the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 402 BP; 72 A; 121 C; 102 G; 106 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 GGAAGAGCCCTGAAAAGCCA 365
                                                                                                                                                                                                                                                                                                           Wang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGAAAAGCCCTGACAAGCCA 20
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Similarity 90.0%;
                                                                                                                                                                                                              immunology, microbiology, molecular biology and
                                                                                                                                                                                                                                                                                                        Bangur CS,
                                                                                                                                                                                                                                                                                                     Gaiger A;
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microbiology; molecular biology;
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Sequence 502 BP; 131 A; 124 C; 163 G; 84 T; 0 other;

WOS Homo sapiens.  XX  WO200155301-A2.  XX  WO200155301-A2.  XX  YX  Q2-MG-2001; 2000US-017905.  XX  17-JAN-2001; 2000US-017905.  XX  17-JAN-2001; 2000US-018350.  RX  21-FEB-2000; 2000US-018350.  RX  21-JAN-2000; 2000US-021840.  RX  21-JAN-2000; 2000US-021440.  RX  21-JAN-2000; 2000US-0225514.  RX  21-JAN-2000; 2000US-022561.  RX  21-JAN-2000; 200US-022561.  RX  21-JAN-2000; 200US-022561.  RX  21-JAN-2000; 200US-022561.  RX  21-JAN-2000; 200US-02560.	ABS40992 ID AAS40992 standard; cDNA; 1444 BP.  XX AAS40992; XX AAS40992; XX CDNA encoding novel human enzyme polypeptide #208.  XX Language isomerase; bydrolase; lyase; isomerase; XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; XX Human; oxidoreductase enzyme; transferase; immunodeficiency disorder; infectious disorder; metabolic disorder; infectious disorder; gene therapy; cytostatic; XX blood-related disorder; infectious disorder; gene therapy; cytostatic; XX blood-related disorder; infectious disorder; gene therapy; cytostatic; XX anti arthritic; nephrotropic; anticoagulant; ss.	Query Match 84.0%; Score 16.8; DB 25; Length 502;  Query Match 90.0%; Pred. No. 87; 2; Indels 0; Gaps 0;  Best Local Similarity 90.0%, Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Mismatches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Mismatches 2; Indels 0; Gaps 0; Mismatches 2; Indels 0; Mismatches 2;
PR 29-SEP-2000; 2000US-0236367, PR 29-SEP-2000; 2000US-0236369, PR 29-SEP-2000; 2000US-0236370, PR 29-SEP-2000; 2000US-0236370, PR 29-SEP-2000; 2000US-0236370, PR 29-SEP-2000; 2000US-0237039, PR 29-SEP-2000; 2000US-0237039, PR 29-SEP-2000; 2000US-0237039, PR 29-CCT-2000; 2000US-0241785, PR 29-CCT-2000; 2000US-0241786, PR 20-CCT-2000; 2000US-0244677, PR 20-CCT-2000; 2000US-0246476, PR 20-CCT-2000; 2000US-0246477, PR 20-CCT-2000; 2000US-0246478, PR 20-CCT-2000; 2000US-0246523, PR 20-CCT-2000; 2000US-0246523, PR 20-CCT-2000; 2000US-0246611, PR 20-CCT-2000; 2000US-0246220, PR 20-CCT-2000; 2000US-0246220, PR 20-CCT-2000; 2000US-0249210, PR 20-CCT-2000; 2000US-0249210, PR 20-CCT-2000; 2000US-0249211, PR 20-CCT-2000; 2000US-0249211, PR 20-CCT-2000; 2000US-0249211	SEP-200 SEP-200	P-2000 P-2000 P-2000 P-2000 P-2000 P-2000 EP-2000 EP-2000 EP-2000 EP-2000 EP-2000

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RESULT 5
AAQ22695
                                                                                                                                                                                     The present invention relates to the isolation of novel human enzyme CC polypeptides (AAUZ2915-AAUZ3814), and the cDNA and genomic sequences controlled classes of controlled classes of the invention may comprise the controlled classes or ligases. The sequences of the invention may comprise the CC diagnosis, treatment, prevention and/or prognosis of a wide range of CC diagnosis, treatment, prevention and/or prognosis of a wide range of CC diagnosis, including hyperproliferative disorders (e.g. cancer), CC (e.g. arthritis), neurological disorders (e.g. cancer), CC (e.g. arthritis), neurological disorders (e.g. Alos) autoimmune disorders (e.g. arthritis), reproductive (e.g. altheimer's disease), CC (e.g. infertility) and infectious disorders (e.g. altheimer's disease), CC (e.g. infertility) and infectious disorders (e.g. altheroselerosis), CC polymucleotides of the invention can also be used in gene therapy. CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published not sequences.
                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                         Matches
                                                                                                                                                       Sequence 1444 BP; 432 A; 284 C; 325 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-2000; 2000US-0251856

08-DEC-2000; 2000US-0251868

08-DEC-2000; 2000US-0251869

08-DEC-2000; 2000US-0251989

11-DEC-2000; 2000US-0251990

11-DEC-2000; 2000US-0251990

05-UAN-2001; 2001US-0254997

05-UAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID No 218; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAU23122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000; 2000US-0249264
17-NOV-2000; 2000US-0249265
17-NOV-2000; 2000US-0249297
17-NOV-2000; 2000US-0249297
17-NOV-2000; 2000US-0249299
17-NOV-2000; 2000US-0249300
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17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                          960 GCAAAGGCCCTGACAAGCCA 979
                                                                                                                     18;
                                                                        1 GGAAAAGCCCTGACAAGCCA 20
                                                                                                             h 84.0%; Score 16.8; DB 22; Similarity 90.0%; Pred. No. 1e+02;
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2000US-0251030.
2000US-0251988.
2000US-0256719.
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                                                                                                  Mismatches
                                                                                           2; Indels
                                                                                                                     Length 1444;
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FF XX XX XX EF
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                              Homo sapiens.
                                   C-metabolism; tumour; pyruvate; T-lymphocyte; ss
                                                         Mitochondrial NAD(P)+-dependent malate enzyme.
                                                                                    31-JUL-1992 (first entry)
                                                                                                              AAQ23258;
                                                                                                                        AAQ23258 standard; DNA; 1923 Bp.
                                                                                                                                                                                                                                                             The inventors claim mitochondrial NAD(P)+-dependent malate enzyme and DNA encoding it. AAR21845 has 5, and 3, non-coding regions. The enzyme catalyses conversion of malate to pyruvate. Both the DNA endividing cells, esp. pyruvate formation metabolism in rapidly (Updated on 25-MAR-2003 to correct PA field.)

(Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                              Sequence 1752 BP; 562 A; 326 C; 386 G; 478 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 12-13; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                Human mitochondrial NAD(P)-dependent malate enzyme - used to study formation of pyruvate from aminoacid(s) in tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR21845.
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-089407/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dworkin MB, Leob , Leober G,
                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BOEH ) BOEHRINGER INGELHEIM.
                                                                                                                                                                         1483 GCAAAGGCCCTGACAAGCCA 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carbon metabolism; pyruvate formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding mitochondrial NAD(P)+-dependent malate enzyme.
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24-JUL-1992
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                                                                                                                                                                                     1 GGAAAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                              Similarity
  Location/Qualifiers
90..1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
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91DE-4120178.
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                                                                                                                                                                                                                     84.0%; Score 16.8;
90.0%; Pred. No. 1e
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                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Krystek E, Maurerfogy I;
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. 1e+02;
2;
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Page σı

mat\_peptide sig\_peptide

/\*tag= b 150..1844

/\*tag= c 1905..1910

/note= "homologous to poly(A) signal AATAAA"

/product= malate\_enzyme 90..149

polyA\_signal

WO9204448-A

23-AUG-1991; 19-MAR-1992.

19-JUN-1991; 08-SEP-1990;

91DE-4120178. 90DE-4028618. 91WO-EP01602

(BOEH ) BOEHRINGER INGELHEIM

Loeber G, Krystek E, Maurerfog I

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22-SEP-2000; 2000US-234567P.
25-SEP-2000; 2000US-234923P.
25-SEP-2000; 2000US-235924P.
25-SEP-2000; 2000US-235077P.
25-SEP-2000; 2000US-235134P.
25-SEP-2000; 2000US-235280P.
25-SEP-2000; 2000US-235238P.
26-SEP-2000; 2000US-235638P.
26-SEP-2000; 2000US-235638P.
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20-SEP-2000;
22-SEP-2000;
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05-JUN-2000; 2000US-209531P.
18-SEP-2000; 2000US-233133P.
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                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2000; 2000US-237316P.
03-OCT-2000; 2000US-237425P.
03-OCT-2000; 2000US-237598P.
03-OCT-2000; 2000US-237604P.
03-OCT-2000; 2000US-237606P.
03-OCT-2000; 2000US-237608P.
03-OCT-2000; 2000US-244867P.
01-NOV-2000; 2000US-244867P.
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28-SEP-2000;
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28-SEP-2000; 2000US-236034P.
28-SEP-2000; 2000US-236109P.
28-SEP-2000; 2000US-236111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2000;
02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-2000;
The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (given in ABL61664 expression of at least 95% identical to (S), where a change in comprises a sequence (S) selected from 847 sequences (divention of BL70110), or is at least 95% identical to civity. (I) has cytostatic to ABL70110, and can be used in gene therapy. MI can be used for screening expression is indicative of anti-neoplastic agent which activity and can be used in gene therapy. MI can be used for product which are in the data collected with respect to the anti-neoplastic agent as a is the data collected with respect to the activity and can be used in the structure and/or properties of the agent. MI can be used in the
                                                                                                                                                                                                                                                                                                                                                     (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                    screening for anti-neoplastic agent involves exposing cells to a screening for anti-neoplastic artivity, and chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                           soppet DR,
                                                                                                                                                                                                                                                                                                                        Young PE,
                                                                                                                                                                                          Claim 1; SEQ ID 5553; 44pp; English.
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2000US-234052P
2000US-234509P
2000US-234567P
2000US-234923P
2000US-234923P
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2000US-233133P.
2000US-233617P.
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2000US-235720P.
2000US-235840P.
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Weaver Z;
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                                                                                                                                                                                                                                                                                                                                       Carter KC,
                                                                                                                                                                                                                                                                                                                                          Ebner R, Endress G,
                                                                                                                                                                                                                                                                                                                                                       Horrigan
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Dworkin MB,

WPI; 1992-114355/14.

P-PSDB; AAR22356.

New human mitochondrial malate enzyme and DNA encoding it for the first studying carbon metabolism in cells, also specific antibodies

purificn. and assay

Claim 1; Page 46 + Fig 3; 60pp; German.

The sequence may be used to study C-metabolism in rapidly dividing

(tumour) cells, esp. pyruvate from the supernatant of mitochondrial (tumour) cells, esp. pyruvate from the supernatant of mitochondrial The enzyme was first isolated from the supernatant of mitochondrial preparations from the transformed human T-lymphocyte cell line preparations from the transformed human T-lymphocyte cell line preparations from the transformed human T-lymphocyte and used as a preparation of oligonucleotides. These were used in PCR basis for the design of oligonucleotides. These were subcloned for amplification of malate enzyme encoding DNA in a CDNA bank for amplification of malate enzyme sendents were subcloned for amplification of malate enzyme the fibrosarcoma bank. In pUC18, sequenced and used to probe the fibrosarcoma bank. A 1923bp insert was isolated and cloned in Bluescript KS+.

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1572 GCAAAGGCCCTGACAAGCCA 1591

1 GGAAAAGCCCTGACAAGCCA 20

Query Match Best Local S

18; Conservative

Similarity

84.0%;

Score 16.8; DB 13; pred. No. 1e+02; 0; Mismatches 2;

, 2; Indels

0

Gaps

Length 1923;

Sequence 1923 BP; 598 A; 373 C; 436 G; 516 T; 0 other; The poly(A+) tail is not included in this sequence.

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ABL67216 standard; DNA; 1923 BP

ABL67216;

15-MAY-2002 (first entry)

Thyroid cancer related gene sequence SEQ ID NO:5553.

stomach; lung; cytostatic; ger gene; ds.

WO200194629-A2. Homo sapiens. Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; wilm's tumour; adenocarcinoma; cytostatic; gene therapy; antineoplastic; wilm's

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The invention relates to novel genes (ABL89449-ABL90853) and proteins CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast (CC and ovarian cancer and other cancers of the adrenal gland, bone, bone CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune (CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune (CC (disease, multiple sclerosis, rhemmatoid arthritis and ulcerative (cC (d) wound healing, (e) neurological disease e.g. cerebral anoxia and (f) infections.

CC (d) wound healing, (e) neurological diseases e.g. cerebral anoxia and (f) infections diseases such as wycardial ischaemias, fungal content of the sequence data for this material, bacterial, fungal
Note: The sequence data for this patent did not form part of the
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                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 433; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                  Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABB89462.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-122018/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-2000; 2000US-205515P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAY-2001; 2001WO-US16450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral, antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL89871 standard; cDNA; 1963 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1923 BP; 599 A; 373 C; 436 G; 515 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
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90.0%; Pred. No. 1e+02;
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26-JUL-2000; 2000US-0220963

14-AUG-2000; 2000US-0220964

14-AUG-2000; 2000US-0224518

14-AUG-2000; 2000US-0224519

14-AUG-2000; 2000US-0225213

14-AUG-2000; 2000US-0225213

14-AUG-2000; 2000US-0225214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US01239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficelency disorder; autoimmune disorder; neurological disorder; metabolic disorder; bioflammatory disorder; cardiovascular disorder; metabolic disorder; blood-related disorder; infectious disorder; reproductive disorder; anti arthritic; nephrotropic; anticoagulant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155301-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding novel human enzyme polypeptide #207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS40991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS40991 standard; cDNA; 2390 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1963 BP; 622 A; 365 C; 394 G; 581 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
; 2000US-0226279;
; 2000US-0226681;
; 2000US-0226868;
; 2000US-0227182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 960 GCAAAGGCCCCTGACAAGCCA 979
                                                                      ; 2000US-0225266
; 2000US-0225267
; 2000US-0225268
; 2000US-0225270
; 2000US-0225447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGAAAAGCCCTGACAAGCCA 20
                                           2000US-0225759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                 200005-0179065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%; Score 16.8;
90.0%; Pred. No. 1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             le+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length 1963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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23-AUG-2000; 30-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 05-SEP-2000; 06-SEP-2000;

2000US-0229345. 2000US-0229344.

2000US-0227009. 2000US-0228924. 2000US-0229287. 2000US-0229343.

06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 12-SEP-2000;

2000US-0231244. 2000US-0231413.

2000US-0229513. 2000US-0230437. 2000US-0230438. 2000US-0231242. 2000US-0231243.

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The present invention relates to the isolation of novel human enzyme CC polypeptides (AMUZ2915-AAUZ3814), and the cDNA and genomic sequences concluding them. The enzyme polypeptides of the invention may comprise the cCC encoding them. The enzyme polypeptides of the invention may comprise the cCC functional classes of oxidoreductases, transferases, hydrolases, lyases, cCC diagnosis, treatment, prevention and/or prognosis of a wide range of CC diagnosis, treatment, prevention and/or prognosis of a wide range of CC diagnosis, treatment, prevention and/or prognosis of a wide range of CC quisonesse including hyperproliferative disorders (e.g. cancer), CCC disorders including hyperproliferative disorders (e.g. cancer), CCC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), CCC (e.g. arthritis), candiovascular disorders (e.g. Alzheimer's disorders (e.g. arthritis), candiovascular disorders (e.g. atherosclerosis), CCC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), The CCC plood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The CCC plood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza) human CCC AAS40785-AAS41684 represent cDNA sequences encoding for the movel human CCC ange polypeptides of the invention.

CCC sequence data for this patent did not form part of the printed cryst production, but was obtained in electronic format directly from WIPO at figure at figure and polypeptides of the grant disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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                            δ
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
                                                                               Query Match
Best Local Similarity
                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptides and polymucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous pulmonary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAU23121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID No 217; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases
                                                                                                                         Sequence 2390 BP; 764 A; 441 C; 488 G; 697 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-465566/50.
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0249210.
2000US-0249211.
2000US-0249212.
2000US-0249213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0249215.
2000US-0249216.
2000US-0249217.
2000US-0249218.
2000US-0249244.
2000US-0249245.
2000US-0249245.
2000US-0249265.
2000US-0249265.
2000US-0249267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0244930
2000US-0250160
2000US-0250160
2000US-0250391
2000US-0251930
2000US-0251930
2000US-0251930
2000US-0251479
2000US-0251479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0251989.
2000US-0251990.
2000US-0254097.
2000US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0251856.
2000US-0251868.
2000US-0251869.
                                                                 Conservative
                                                                                      84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM;
                                                                         0;
                                                                        Score 16.8; DB 22;
Pred. No. 1.1e+02;
p; Mismatches 2;
                                                                                                                Length 2390;
                                                                                       0
                                                                                           Gaps
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2000US-0236370.

2000US-0239937. 2000US-0240960.

2000US-0241809.

08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

2000US-0244617.
2000US-0246474.
2000US-0246475.
2000US-0246477.
2000US-0246477.
2000US-0246528.
2000US-0246524.
2000US-0246527.
2000US-0246528.
2000US-0246529.
2000US-0246613.
2000US-0249208.
2000US-0249208.

0

08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 17-NOV-2000;

14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

2000US-0232401 2000US-0233063 2000US-0233065 2000US-0234223 2000US-0234274 2000US-0234297 2000US-0234997 2000US-0234984 2000US-0235883 2000US-0235834 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836

14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

14-SEP-2000; 14-SEP-2000;

2000US-0232399. 2000US-0232400. 200005-0232398.

2000US-0231968. 2000US-0232397.

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RESULT 11
AAS40590
                                                                                                                                            The present sequence encodes a novel protein kinase. The nucleic acids CC and the protein kinases they encode may be used in the treatment and CC diagnosis of diseases associated with inappropriate kinase expression cc such as immune-related diseases and disorders, cardiovascular disease, cc complementary sequences may also be used as DNA probes in diagnostic CC assays. The kinase expression and activity also be used as DNA probes in diagnostic CC and kinase expression and activity. Anti-kinase antibodies of kinase expression and activity. Anti-kinase antibodies CC artivity include rheumatoid arthritis, atherosclerosis, autoimmune CC disorders, complications of organ transplantation, myocardial infarction, CC contonic inflammatory pelvic disease, strokes, renal failure, chronic inflammatory pelvic disease, multiple sclerosis, asthma, cc reproductive disorders, rhinitis, autoimmunity, diabetes, cancers and
                                                                                                   Matches
                                                                                                                    Query Match
                                                                                                                          Sequence 2463 BP, 622 A; 686 C; 706 G; 447 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding kinase polypeptides, useful for diagnosing and reating immune-related diseases and disorders, cardiovascular disease,
                                                                                                            Local
                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2; 310pp; English.
                                                                                                                                                                                                                                                                                                                                            neurodegenerative diseases and/or cancers
                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB65702
                                                                                                                                                                                                                                                                                                                                                                                                                      Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000WO-US14842.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease;
                                                             2031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200073469-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protein kinase cDNA, SEQ ID NO: 112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF44731 standard; cDNA; 2463 BP.
                                                                       1 GGAAAAGCCCCTGACAAGCCA 20
                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                  2001-032161/04.
                                                                                                        Similarity
                                                     GGCAAAGCCCTCACAAGCCA 2050
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Martinez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0136503.
                                                                                               84.0%; Score 16.8; DB 22; 90.0%; Pred. No. 1.1e+02;
                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                           Whyte D, Sudersanam S;
                                                                                         Mismatches
                                                                                     Indels
                                                                                                      Length 2463;
                                                                                   0;
                                                                                Gaps
                                                                                0,
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31-JAN-2000; 2000US-0179065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001; 2001WO-US01239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200155301-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding novel human enzyme polypeptide #206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS40990 standard; cDNA; 3085 BP
2000US-0232080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000US-0220964.
; 2000US-0224518.
; 2000US-0224519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0217486

2000US-0215135

2000US-021647

2000US-021680

2000US-0217487

2000US-0217487

2000US-0217487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000US-0184664
; 2000US-0186350
; 2000US-0189874
; 2000US-0190076
; 2000US-0198123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0225214.
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08-SEP-2000; 2000US-0232081. 12-SEP-2000; 2000US-0231968. 14-SEP-2000; 2000US-0232397.

14-SEP-2000;

2000US-0233063 2000US-0233064 2000US-0233065 2000US-0233065 2000US-0234223 2000US-0234274 2000US-0234297 2000US-0234991 2000US-0234998

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XX
The present invention relates to the isolation of novel human enzyme
CC
polypeptides (AAUZ2915-AAUZ3814), and the cDNA and genomic sequences
CC
encoding them. The enzyme polypeptides of the invention may comprise the
CC
encoding them. The enzyme polypeptides of the invention may comprise the
CC
encoding them. The enzyme polypeptides of the invention may comprise the
CC
encoding them. The sequences of the invention are useful in the
CC
disonerases or ligases. The sequences of the invention are useful in the
CC
encoding them. The sequences of the invention are useful in the
CC
disorders including hyperproliferative disorders (e.g. cancer),
CC
encoding hyperproliferative disorders (e.g. cancer),
CC
encoding hyperproliferative disorders (e.g. cancer),
CC
encoding hyperproliferative disorders (e.g. Alzheimer's disease),
CC
encoding hyperproliferative disorders (e.g. Alzheimer's disease),
CC
encoding hyperproliferation disorders (e.g. Alzheimer's disease),
CC
encoding hyperproliferation disorders (e.g. atherosclarosis),
CC
encoding hyperproliferation disorders (e.g. atherosclarosis),
CC
encoding hyperproliferation disorders (e.g. influenza) The
CC
controlled disorders (e.g. haemophilia), reproductive disorders
(e.g. asthma), cardiovascular disorders (e.g. influenza) The
CC
encoding hyperproliferation disorders (e.g. influenza) The
controlled disorders (e.g. haemophilia), reproductive disorders
(e.g. asthma), cardiovascular disorders (e.g. influenza) The
cc
cc encoding hyperproliferation disorders (e.g. influenza) The
cc encoding hyperproliferation disorders (e.g. theroscaleration disorders (e.
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01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-025198.
05-DEC-2000; 2000US-025198.
05-DEC-2000; 2000US-0251479.
06-DEC-2000; 2000US-0251479.
06-DEC-2000; 2000US-0251866.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251990.
08-DEC-2000; 2000US-0251990.
08-DEC-2000; 2000US-0251990.
08-DEC-2000; 2000US-0251990.
08-DEC-2000; 2000US-0254097.
11-DEC-2000; 2000US-0254097.
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RESULT 12
                                                                                                                                                                                                                                                               AAT91285
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-465566/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID No 216; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3085 BP; 948 A; 579 C; 652 G; 905 T; 1 other;
                                                                                                                                                                                                                                            AAT91285 standard; DNA; 180 BP.
                                                                                                                                                                                                     AAT91285;
                   Neutral protease; npr gene; enzyme engineering; protein engineering; lactic acid bacterium; food; milk; cheese; ripening; Bacillus subtilis; promoter; ss.
                                                                                                          Lactococcal promoter P23.
                                                                                                                                                       27-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal
                                                                                                                                                                                                                                                                                                                                                      1668 GCAAAGGCCCTGACAAGCCA 1687
                                                                                                                                                                                                                                                                                                                                                                                 1 GGAAAAGCCCTGACAAGCCA 20
| ||| ||||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8;
pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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08-NOV-2000; 2000US-0246476.
08-NOV-2000; 2000US-0246477.
08-NOV-2000; 2000US-0246523.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246524.
08-NOV-2000; 2000US-0246526.
08-NOV-2000; 2000US-0246527.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246528.
08-NOV-2000; 2000US-0246610.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0246611.
08-NOV-2000; 2000US-0249207.
17-NOV-2000; 2000US-0249207.
17-NOV-2000; 2000US-0249211.

21-SEP-2000; 2000US-0234223.
21-SEP-2000; 2000US-0234997.
25-SEP-2000; 2000US-0234998.
25-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236368.
29-SEP-2000; 2000US-0236369.
29-SEP-2000; 2000US-0236370.
29-SEP-2000; 2000US-0236370.
29-CCT-2000; 2000US-0237037.
02-CCT-2000; 2000US-0237037.
02-CCT-2000; 2000US-0237039.
02-CCT-2000; 2000US-0237039.
02-CCT-2000; 2000US-0237039.
02-CCT-2000; 2000US-0237039.
03-CCT-2000; 2000US-0237039.
03-CCT-2000; 2000US-0241786.
20-CCT-2000; 2000US-0241786.
20-CCT-2000; 2000US-0241809.
20-CCT-2000; 2000US-0244874.
08-NOV-2000; 2000US-0244674.
08-NOV-2000; 2000US-0244674.

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ABN6933
                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                           Matches
                                                                                                                                                                                                           Query Match
 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                             Streptococcus polynucleotide SEQ ID NO 6585.
                                                                         01-JUL-2002
                                                                                                    ABN69336 standard; DNA; 936 BP
                                                                                           ABN69336;
                                                                                                                                                                                                                               This sequence comprises lactococcal promoter P23, which was obtained from plasmid pckV223 by PCR amplification, and which has been inserted into pck10 upstream of the Bacillus subtilis neutral protease npr gene (see AAT91284) to yield pck12. Lactococcal used to control expression of the B. subtilis neutral constructs used for transformation of lactic acid bacterial strains. The npr gene can be engineered to code for an enzyme strains. The npr gene can be engineered to code for an enzyme (see neutral protease properties of the bacterium transformant allows the intended application. The method is especially used to cheese maritima.
                                                                                                                                                                                                               Sequence 180 BP; 85 A; 22 C; 31 G; 42 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 5; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Bio-transformation of a substrate using modified lactic acid bacterium - which contain a gene encoding altered neutral protease
                                                                                                                                                                                                  Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-535460/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FRIE-) FRIESLAND BRANDS BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9738587-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sgo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus sp.
                                                                                                                                                        w
                                                                                                                                                            2 GAAAAGCCCTGACAAGCC 19
                                                                                                                                                                                               Similarity
                                                                                                                                               GAAAAGCCCTGACAACCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                Mierau I, Van Den Burg L,
                                                                    (first entry)
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96EP-0200948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-NL00192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "5' end of coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
136..144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
88..93
                                                                                                                                                                                     82.0%; Score 16.4; DB 18; 94.4%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154..180
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                                                                                                                                                                               Mismatches
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                                                                                                                                                                            Indels
                                                                                                                                                                                           Length 180;
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XXX WXX DXX
                                                                                                                               RESULT 14
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                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                          Query Match
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                                                                                          AAA26448;
                                                                                                                                                                                                 Local
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AX EX EX EX AX A

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The invention relates to a protein (ABP25413-ABP30895) from group B CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for CC the treatment or prevention of infection or disease caused by the treatment or prevention of infection or disease caused by CC Nucleic acids encoding (I) are used in detertable and S. pyrogenes. (CC (I). A composition comprising (I) or a nucleic streptococcus in a CC used as a vaccine or disgnostic composition. The disease caused by CC streptococcus that is prevented or treated may be mentingitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be constant of the constant of th
Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antilly, antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour; ss.
                                                                                                                                                                                                                                                    Human secreted protein gene 20 SEQ ID NO:113.
                                                                                                                                                                                                                                                                                                                                                    29-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA26448 standard; cDNA; 2214 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 936 BP; 294 A; 180 C; 168 G; 294 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 3821; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549 GAAAAGCCCTGACAAGAC 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200234771-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAAAAGCCCTGACAAGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.0%; Score 16.4; DB 24; 94.4%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 936;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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cc antiallergic; descepathic; antiarthitic, antibacterial; antidabetic; cantialergic; descepathic; antiarthitic; antibacterial; antidiabetic; corresponding secreted proteins are useful for preventing, treating or corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also ameliorating medical conditions, e.g. by protein or gene therapy. Also conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the complymucleotides, based on which tissues they are most highly expressed complymucleotides, based on which tissues they are most highly expressed complymucleotides, based on which tissues they are most highly expressed composition, and include developing products for the diagnosis or treatment of control of the control of the immune system, and foetal deficiencies, blood disorders, developmental abnormalities cantoimmune diseases, hepatic and renal diseases of the immune system, control of the physical condition, control of the physical condition, control of the proteins of the proteins of the proteins candiovascular disorders, asthma, sepsis, and, pastrointestinal candiovascular disorders, respiratory disorders and metabolic disorders. The proteins control of the proteins are also used as food additives or preservatives. CC analogament of the proteins of
                                                                                                                                                                                                     5
                                                                                        RESULT 15
                                                                                                                                                             밁
                                                               ACC50730
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                     Query Match
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06-AUG-1998;
12-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1998;
05-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in Examples of the activities are: cytostatic; neuroprotective; immunosuppressive; antiinflammatory; nootropic; neuroprotective; immunosuppressive; activities are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, immune diseases, inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lafleur D, Wei Y, Ni o
Soppet DR, Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komatsoulis GA, Ro
Lafleur D, Wei Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 443; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-195282/17.
                                                                                                                                                                                                                                                                                                                                                Sequence 2214 BP; 528 A; 540 C; 554 G; 569 T; 23 other;
ACC50730;
                                             ACC50730 standard; cDNA; 2214 BP
                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                  305 GGGRARGGCCTGACAAGCCA 324
                                                                                                                                                                                        1 GGAAAAGCCCTGACAAGCCA 20
|| :|:| |||||||||||
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                          Conservative
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Y, Ni J, Florence
                                                                                                                                                                                                                                                                                      80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM,
                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                      Score 16; DB 21; | Length 2214; Pred. No. 2.7e+02;
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A, Young PE, Brewer LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mucenski M
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The present invention relates to novel human secreted proteins CC (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The CC (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The CC cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, CC cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, CC coronary arteriosclerosis and myocardial ischaemia), neural disorders, CC coronary arteriosclerosis and myocardial ischaemia), neural disorders, CC coronary arteriosclerosis, pulmonary disorders, renal disorders, CC quastrointestinal disorders, pulmonary disorders, renal disorders, CC quastrointestinal disorders and/or cancerous disease and conditions, for CC proliferative disorders and/or cancerous diseases and conditions or CC proventing neural damage which occurs in neuronal disorders or CC preventing neural damage which occurs in neuronal disorders or preventing neural damage which occurs in neuronal disorders or company disease, to enhance bone and pariodontal regeneration and aid in tissue CC transplants or bone grafts, to prevent skin aging or hair loss, to crass the company of the company of
                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
vulnerary; antiinflammatory; nootropic; neuroprotective;
antiparkinsonian; gene therapy; human; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein coding sequence, SEQ ID 397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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19-JUL-2001; 2001US-306171P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-2002; 2002WO-US09785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-2001; 2001US-331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; SEQ ID 397; 1881pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                             embryonic stem cells, or to modulate mammalian characteristics or
                                                                                                                                                                                             Sequence 2214 BP; 528 A; 540 C; 554 G; 569 T; 23 other;
                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                       Note: The sequence data for this patent was published in electronic format and is available from WIPO at
305
                                              1 GGAAAAGCCCTGACAAGCCA 20
                                                                                              16; Conservative
                                                                                                                            Similarity
GGGRARGGCCTGACAAGCCA 324
                                                                                                                            80.0%; Score 16; DB 25;
80.0%; Pred. No. 2.7e+02;
                                                                                                         2; Mismatches
                                                                                                                                                             DB 25; Length 2214;
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Search completed: August 1, 2003, 13:55:13

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Job time : 8.69868 secs

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OM nucleic - nucleic search, using sw model

August 1, 2003, 08:05:17 ; Search time 5.18607 Seconds

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perfect score: Scoring table:

US-09-834-291-6 20

ggaaaagccctgacaagcca 20

IDENTITY\_NUC Gapext 1.0

1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0
Maximum DB seg length: 2000000000 Post-processing: Minimum Match 0%

Listing first 45 summaries

Match 100%

Result

Score

Match Length DB

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SUMMARIES

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266 9 720 9 2380 9 2827 9 3212 1923 1923 824 9025608 438 9025608 438 606

US-09-834-291-6
9 US-09-834-291-7
9 US-09-834-291-10
9 US-09-834-291-32
9 US-09-834-291-32
9 US-09-834-291-32
9 US-09-834-291-33
9 US-09-834-291-4
9 US-09-834-291-4
9 US-09-834-291-1
13 US-10-027-632-134797
13 US-10-156-761-1
14 US-09-18-995-1098
11 US-09-18-995-1098
12 US-09-866-108-15724
9 US-09-866-108-15724
9 US-09-866-108-15724
9 US-09-866-108-15724
9 US-09-866-108-15724

Searched:

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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sequence 7, Appli
sequence 10, Appl
sequence 10, Appl
sequence 24, Appli
sequence 27, Appli
sequence 27, Appli
sequence 3, Appli
sequence 4, Appli
sequence 1, Appli
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sequence 134797,
sequence 134797,
sequence 10399, A
sequence 15724, A
sequence 15724, A
sequence 137408,
                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09834291

Sequence 6, MS20020042064A1

Patent No. US20020042064A1

GENERAL INFORMATION: Peter
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
APPLICANTON INTEREST US/09/834,291
FILE REFERENCE: 4121-122

FURRENT APPLICATION NUMBER: US/09/834,291
CURRENT APPLICATION NUMBER: PCT/DE99/03343

PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-16
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LENGTH: 20
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US-09-834-291-5
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Best Local S:
                          Sequence 5, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
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13 US-10-027-632-8488
13 US-10-027-632-137414
13 US-10-027-632-137414
13 US-10-027-632-137414
14 US-09-764-847-1628
14 US-09-764-847-1628
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10 US-09-764-847-1629
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14 US-09-764-869-1734
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18 US-09-764-891-9685
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11 US-10-027-632-111067
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18 US-10-198-846-4234
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10 US-09-933-291-9
10 US-09-933-291-9
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Sequence 137413,
Sequence 137414,
Sequence 1627, Ap
Sequence 1628, Ap
Sequence 1628, Ap
Sequence 312, App
Sequence 312, App
Sequence 312, App
Sequence 1629, Ap
Sequence 1629, Ap
Sequence 1734, Ap
Sequence 1734, Ap
Sequence 1734, Ap
Sequence 265, Ap
Sequence 366, App
Sequence 366, App
Sequence 366, App
Sequence 31066,
Sequence 111067,
Sequence 111067,
Sequence 11087,
Sequence 10892, Ap
Sequence 10892, Ap
Sequence 10892, Ap
Sequence 111067,
Sequence 111067,
Sequence 10892, Appli
Sequence 10892, Appli
Sequence 1, Appli
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Sequence 9, Appli
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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
FITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT FILLING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
                                                                                                                               Sequence 10, Application US/09834291
Fatent No. US20020042064A1
GENERAL INFORMATION:
                                                                                                                                                                                         US-09-834-291-10
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVESTION: DS3 Binding Areas
CURRENT FALLOR 1421-122
CURRENT FALLOR DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US/09/834,291
PRIOR APPLICATION NUMBER: D61-21
PRIOR APPLICATION NUMBER: D61-29/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ODCANITON.
                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo Sapiens
US-09-834-291-7
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US-09-834-291-5
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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                                                                                                                                                                                                                                                                                                                          Local Similarity
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
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95.0%; Pred. No. 9.
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GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
ITILE OF INVENTION: p53 Binding Areas
CURRENT APPLICATION D53 BINDING AREA
CURRENT APPLICATION NUMBER: US/09/834,291
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
SEQ ID NO 32
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                           RESULT 6
US-09-834-291-32
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Patent No. US20020042064A1
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APPLICANT: Muller-Schilling, Martina
TITLE OF INVENTION: P53 Binding Areas
FILS REFERENCE: 4121-122
CURRENT FILING DATE: 2001-08-9/834,291
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
NUMBER OF SEQ ID NOW: 32
NUMBER OF SEQ ID NOW: 32
NUMBER OF SEQ ID NOW: 32
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SEQ ID NO 24
LENGTH: 20
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SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-10
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Patent No. U
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapiens
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PRIOR APPLICATION NUMBER: DE 198 47 779.1
NUMBER OF SEQ ID NOS: 32
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US20020042064A1
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95.0%; Pred. No. 9.3;
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Pred. No. 9.3;
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US-09-834-291-32
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GENERAL INFORMATION:
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: PCT/DE99/03343
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR APPLICATION NUMBER: DE 198 47 779.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Krammer, Peter APPLICANT: Muller-Schilling, Martina APPLICANT: Oren, Moshe
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                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09834291
PATENT NO. US20020042064A1
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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                                                         US-09-834-291-3
                                                                                                                                                                                 TITLE OF INVENTION: p33 binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR PILING TON NUMBER: DE 198 47 779.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                         SEQ ID NO 3
                        Query Match
                                                                                                                                                       PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 720
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                         SOFTWARE:
                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                           ENGTH: 2380
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 y Match 92.0%; Score 18.4; D
Local Similarity 95.0%; Pred. No. 10;
Local Similarity 95.0%; Mismatches
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Similarity 95.0%; Score 18.4; DB 9;
Similarity 95.0%; Pred. No. 9.8;
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Similarity 95.0%;
                                                                                                                                          PatentIn Ver. 2.1
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Conservative
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pred. No. 1
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                                        DB 9; Length 2380;
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            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                      APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
APPLICANT: Oren, Moshe
TITLE OF INVENTION: D53 Binding Areas
TITLE OF INVENTION: D53 Binding Areas
TITLE APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 1998-10-18
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; sequence 1, Application US/09834291 patent No. US20020042064A1 GENERAL INFORMATION:
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TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
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PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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SEQ ID NO 1
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2827
                                                                        Matches
                                                                                                           Query Match
                                                                                                                                                                     TYPE: DNA ORGANISM: Homo Sapiens
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                                                                                           Local Similarity
2659 ĠĠĀCĀĀĠĊĆĊŢĠĀĊĀĀĠĊĊĀ 2678
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                                                                            Conservative
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95.0%; Pred. No. 1
                                                                                                 92.0%; Score 18.4;
95.0%; Pred. No. 1
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RESULT 11

US-09-964-824A-250

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PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-11-23

PRIOR PPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

INUMBER OF SEQ ID NOS: 325720

SOFTWARE: PASKSQ for Windows Version 4.0

LENGTH. 62,
                        В
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                                                                                                                Matches
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; ORGANISM: Homo sapiens
US-09-964-824A-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 134797, Application US/10027632
GRNERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/027,632
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APPLICANT: HORIGAN, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
PRIOR FILLNG DATE: 2001-09-27
PRIOR FILLNG DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILLNG DATE: 2000-09-28
PRIOR PRIOR DATE: 2000-09-28
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                                                                                                                                                                                                                                                                                      ENGTH: 824
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                                                                                                                                        Local
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694 AAAAGCCCTGAAAAGCCA 677
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                                          3 AAAAGCCCTGACAAGCCA 20
                                                                                                     17; Conservative
                                                                                                                              Similarity
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                                                                                                                82.0%; Score 16.4;
94.4%; Pred. No. 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%; Score 16.8;
90.0%; Pred. No. 67
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                                                                                        Mismatches
                                                                                                                        DB 13; Length 824;
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В
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; ORGANISM: Homo sapiens
US-09-918-995-10989
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PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SEQ ID NO 10989
PRIOR FILING DATE: 1999-01-20
NO 10989
PRIOR FIRESTER FASTSEQ FOR WINDOWS Version 3.0
                                                                                    Matches
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US-09-918-995-10989
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ITITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION UNMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION UNMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10989, Application US/09918995
Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-156-761-1/c
                                                                                                                                                                                                                   LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                           Match 79.0%; Score 15.8; DB 11; Length 438; Local Similarity 89.5%; Pred. No. 1.9e+02;
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383 GAAAAGGCCTGACAAGACA 401
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                                                                         17; Conservative
                          2 GAAAAGCCCTGACAAGCCA 20
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.0%; Score 16.4;
94.4%; Pred. No. 9;
                                                                     0; Mismatches
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US-09-866-108-15724

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Sequence 13714, Application US/09866108

GENERAL INFORMATION:

APPLICANT GU, YILLDOG
APPLICANT GU, YILLDOG
APPLICANT GU, YILLDOG
APPLICANT GU, YILLDOG
APPLICANT DATE:

APPLICANT PENN, SHATTON G.
APPLICANTON MERRE: US 69/26,359

PENOR APPLICANTON MERRE: PCT/US01/00664

PENOR APPLICANTON MEMBER: PCT/US01/00669

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Maximum DB seq length: 2000000000
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14.4
14.4
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Listing first 45 summaries
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Match
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     Length
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US-09-489-847-113

US-09-276-531-93

US-08-894-997-49

US-09-252-991A-14234

US-09-252-991A-14146

US-09-252-991A-13990

US-09-252-200-88

US-09-232-200-88

US-09-232-201-88

US-09-232-201-88

US-09-232-201-88
       3 US-09-103-840A-2

3 US-09-133-840A-1

3 US-09-133-840A-1

3 US-09-634-238-1

5 US-09-135-782-1

5 US-09-135-782-1

5 US-09-240-372-1

5 US-09-530-212A-1

5 US-09-564-805-221

6 US-09-911-927-13

8 US-09-911-927-13

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5347.959 Million cell updates/sec
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Sequence 113, App
Sequence 49, Appl
Sequence 49, Appl
Sequence 14234, A
Sequence 14146, A
Sequence 13990, A
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                                                                                                                        Sequence 88, Appl
Sequence 1, Appli
Sequence 21, Appli
Sequence 221, Appli
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Sequence 13, Appl
Sequence 13, Appl
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CURRENT FILING DATE: 1998-12-23
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR PEPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
PRIOR FILING DATE: 1997-12-24
PRIOR FILING DATE: 1917-12-24
PRIOR FILING DATE: 1917-12-24
PRIOR FILING DATE: 1917-12-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-220-132-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Fasu
SEQ ID NO 85
SEQ TH: 1923
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CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
CURRENT FILING DATE: 2000-01-29
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1998-07-29
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-09-,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-12
EARLIER FILING DATE: 1998-08-12
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Best Local S
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APPLICANT: Rosen et al

TITLE OF INVENTION: 98 Human Secreted Proteins

FILE REFERENCE: PZ031P1

FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                sequence 113,
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US-08-311-731A-120
US-08-135-171B-3
US-08-435-998-3
US-09-188-930-8
US-09-197-532A-2050
US-09-107-532A-2050
US-08-107-532A-2050
US-08-131-625B-18
US-08-855-531D-15
US-08-855-531D-15
US-08-855-531D-15
US-08-855-531D-15
US-08-855-731B-5
US-09-252-991A-2613
US-09-252-991A-2613
US-09-328-352-71A-9
US-08-725-027-9
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Pred. No. 12
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sequence 3, Appli
sequence 86, Appl
sequence 2050, Appl
sequence 2050, Appl
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TELEPOMMINICATION INFORMATION:
TELEPHONE: (650) 855-0555
INFORMATION FOR SEQ ID NO: 93:
LENGTH: 72 base pairs
TYPE: nucleid acid
STRANDENDEC: 4111
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FEATURE:
NAME/KEY: SITE
LOCATION: (299)
OTHER INFORMATION: n equals a,t,g, or c
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GENERAL I
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
APPLICATION DATA:
APPLICATION UMBER: US/09/276,531
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 93, Application US/09276531 Patent No. 6183968
                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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Best Local Similarity
                STRANDEDNESS:
                                                                                                                  NAME: Lynn E. Murry, Ph.D.
REGISTRATION NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0008 US
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reddy, Roopa
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
NUMBER OF SEQUENCES: 134
CORPREDAMENTANT RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
NUMBER FILING DATE: 1998-08-06
SOFTWARE: PEO ID NOS: 376
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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linear
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           single
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80.0%; Pred. No. 32;
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ITILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILI
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APPLICANT: Schoenherr, Christopher J
TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
CURRENT APPLICATION NUMBER: US/08/894,997A
CURRENT FILING DATE: 1998-01-06
EARLIER APPLICATION NUMBER: PCT/US96/02817
EARLIER APPLICATION NUMBER: PCT/US96/02817
EARLIER APPLICATION NUMBER: PCT/US96/02817
EARLIER APPLICATION NUMBER: 08/398,590
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PSEC ID NOS: 55
SOFTWARE: PATENTIAN POS: 55
SOFTWAR
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APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent Mo. 6551795
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Best Local ;
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US-09-276-531-93
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PATENT NO. 6270990
GENERAL INFORMATION:
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LOCATION: (1)..(4057)
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Best Local Similarity 89.5
Matches 17; Conservative
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les 17; Conserv
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LIBRARY: BRSTTU
CLONE: 1729463
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89.5%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%; Score 15.8; 89.5%; Pred. No. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _ DB 3; Length 4057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ν
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76.0%; Score 15.2; DB 4; Length 738;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14146, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-13990/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-188
PRIOR FILING DATE: 1998-07-189
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 14146
LENGTH: 1107
                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13990, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                             APPLICANT: MARC J. RUBERfield et al.
APPLICANT: MARC J. RUBERFIELD AND AND ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PRIOR DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
RESULT 8
US-09-232-200-88/c
; Sequence 88, Application US/09232200A
                                                                                                                                                                                                                                                                                    SEQ ID NO 13990
LENGTH: 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                            Matches
                                                                                                                                                                                             Query Match
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                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGAAAAGCCCCTGACAAGCCA 20
                                                                                        739 ĠĠĀĀĀĀĠĠĊĊŦĠĠĊĀĠĠĊĊĀ 720
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                                                                                                                                                                                   Similarity
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85.0%;
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Pred. No. 72;
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                                                                                                                                                                         0
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Pred. No. 77;
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                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; | Indels
                                                                                                                                                                               3; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Lodish, Harvey F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
ITILE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MB
CURRENT APPLICATION NUMBER: US/09/232,200A
CURRENT FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-01-04
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
NUMBER OF SEQ ID NOS: 105
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APPLICANI: CHOCKEN, RUTH E.
APPLICANI: CHOCKEN, RUTH E.
APPLICANI: TARTEGILA, LOUIS A.
APPLICANI: TARTEGILA, LOUIS A.
APPLICANI: TARTEGILA, LOUIS A.
APPLICANI: TARTEGILA, LOUIS A.
APPLICANION: PATTY ACID TRANSPORT PROTEINS
TITLE OF INVENTION: PATTY ACID TRANSPORT PROTEINS
CURRENT APPLICATION NUMBER: 60/09/32,197A
CURRENT FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
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US-09-232-197-88/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                      US-09-232-197-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
                                                                                                                                                                                                                                        SEQ ID NO 88
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                             Matches
                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                TYPE: DNA ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 17; Conserv
                                                                                                 Local Similarity
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46 GGÁAAATCCTTGÁCAAGGCA 27
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                                       1 дальнанскителенания 20
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                                                                               Conservative
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85.0%;
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85.0%;
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Pred. No. 80
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Pred. No. 80;
                                                                                            Mismatches
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US-09-232-201-88/C

RESULT 10

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RESULT 12
US-09-103-840A-1
; Sequence 1, Application US/09103840A
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                                                                                                                                                                     Matches
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                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
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APPLICANT: Gineno, Ruth E.

APPLICANT: Tartagila, Louis A.

TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS

FILE REFERENCE: WHI97-21p3MC

CURRENT FILING DATE: 1999-01-14

EARLIER APPLICATION NUMBER: 60/071,374

EARLIER APPLICATION NUMBER: 60/071,374

EARLIER APPLICATION NUMBER: 60/093,491

EARLIER APPLICATION NUMBER: 60/093,491

EARLIER FILING DATE: 1998-07-20

EARLIER FILING DATE: 1998-07-20

EARLIER FILING DATE: 1998-07-20

EARLIER FILING DATE: 1998-17-20

EARLIER FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORCANISM: Saccharomyces cerevisiae
US-09-232-201-88
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WRITE, Owen R.
APPLICANT: WRITER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                              OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
                                                                                4172848 ĠĠĀĀĀĀĠĊĊĠŦĠĀŦĀĀŦĊĊĀ 4172867
                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 85.0%;
Matches 17; Conservative
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LENGTH: 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88, Application US/09232201A
                                                                                                                                                                 Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
                                                                                                              1 GGAAAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2, Application US/09103840A
3. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 GGAAAATCCTTGACAAGGCA 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                             Conservative
                                                                                                                                                                 76.0%; Score 15.2;
85.0%; Pred. No. 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                      Mismatches
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Pred. No. 8
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                                                                                                                                                                         DB 3; Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1872;
                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                           0,
                                                                                                                                       Gaps
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                                                                                                                                     0,
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B
RESULT 14
                                                                                                                                                      : OTHER INFORMATION: n = A, T, C or G US-09-634-238-137
                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Vers
SEQ ID NO 137
LENGTH: 2221
TYPE: DNA
ORGANISM: Lactobacillus rhamnosus
                                                                                                       Query Match
Best Local Similarity
                                                                                                  Matches
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                                                                                                                                                                                                                                                                             FILE REFERENCE: 11000.1043U1
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Christensson, Anna C.
APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul W.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
ETITE OF INVENTION: them and methods for using them.
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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NAME/KEY: misc feature
LOCATION: (1)...(2221)
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APPLICANT:
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Best Local Similarity
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FILE REFERENCE: 24366-20007.00
CURRENT EPILICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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                              283 GGCAAAGCCCTGACCAGC 300
                                                1 GGAAAAGCCCTGACAAGC 18
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Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
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88.9%;
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85.0%; Pred. No. 98;
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                                                                                          Score 14.8; DB 4; Length 2221; Pred. No. 1.3e+02;
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US-09-135-782-1/c

Sequence 1, Application US/09135782

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US-09-135-782-1
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APPLICANT: Xu, Shuang-yong
APPLICANT: Xu, Shuang-yong
APPLICANT: Shuang-yong
TITLE OF INVENTION: Endonuclease In E. coli And Purification Of The
TITLE OF INVENTION: Endonuclease In E. coli And Purification Of The
TITLE OF INVENTION: Recombinant NapI Restriction Endonuclease
FILE REFERENCE: NEB-143
CURRENT APPLICATION NUMBER: US/09/135,782
CURRENT FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6027929
GENERAL INFORMATION:
                                                                                   US-08-240-372-1
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LOCATION: (1)..(1191)
Best Local Similarity
Matches 15, Conserva
                                        Query Match
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KATO, ELIE K.

APPLICANT: STUART, W. DORSEY
APPLICANT: STUART, W. DORSEY
TITLE OF INVENTION: LIGHT-REGULATED PROMOTERS FOR PRODUCTION
TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS IN FILAMENTOUS FUNGI
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
SOFTWARE: PATENTIAN DATA:
CURRENT APPLICATION NUMBER: US/08/240,372
FILING DATE: 10-MAX-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 3918-0003.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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TEX: 90-4030
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CITY: Washington, D.C.
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STREET: 2000 Pennsylvania Ave. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                            LENGTH: 1237 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                            TOPOLOGY: linear
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                      72.0%; Score 14.4; DB 1; Length 1237; 93.8%; Pred. No. 1.9e+02;
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Search completed: August 1, 2003, 08:37:08 Job time : 13.6507 secs

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OM nucleic - nucleic search, using sw model
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Perfect score:
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Maximum DB seq length: 2000000000
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(without alignments)
10468.541 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

REFERENCE	KEYWORDS SOURCE ORGANISM	RESULT 1 AX026093 LOCUS DEFINITION ACCESSION VERSION	•	45 16				17	17	17 17	17	17	17	17	17.	25 17.	23 17.	17.	<u></u>	19 . 18	18.4	18.4	14 18.4	18.4	20	20	20	20	; 20	20	2 0	20	No. Score	pegult
schilling, M., Kramme	Homo sapiens (human) Homo sapiens Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, V	20 bp DNA AX026093 from Patent DE19847779. AX026093 AX026093.1 GI:10187524	ALIGNMENTS	.8 84.0 20 6 AAV	17 85.0 280469 2 ACCESTS  8 84.0 20 6 AXO26095  .8 84.0 7 7026097	262681	240214	4 87.0 289818	4 87.0 238103 87.0 258131	4 87.0 230097	87.0 223831	87.0 206373	87.0 193347	87.0 186325 87.0 189485	87.0 185049	87.0 166772	87.0 163933	87.0 380	90.0 215973	90.0 145667	90.0 81200 2	92.0 199776 9	93352 2	67412 2	20 6	15121 6	3212 6	2380. 6	720 6	266 9	20 6 AX02	000	IGCE OF ALL	
Oren,M. fving apoptosis-modulating	ta; Vertebrata; Euteleostomi; hini; Hominidae; Homo.	A linear PAT 16-SEP-2000		·	26097 Sequenc	ACI21541 Mus muscu	5569 8975	attus	attus	attus	na mu	AC115292 Mus muscu	AL356606 Homo sapi AL356606 Homo sapi	AC125884 Rattus no	AC074244 Homo sapi	mar	AL589763 Human DNA	AC13997/ Raccus in Ar,929559 Zebrafish	AF444228 Microbotr	AC091422 Mus """" RX511088 Danio rer	, 2	AL732613 FORD Sapi	AC011499 Homo sapi	mus	AL356352 Homo sapi	AL157394 Human Dra-	AX695635 Sequence	AX026092 Sequence	AX026091 Sequence	AX026090 Sequence	26120	O U	26093	ripti

AUTHORS TITLE

Mueller-Schilling,M., Krammer,P. and Oren,M. Novel receptor dna useful for identifying apoptosis-movel receptor dna useful for cancer chemotherapy substances potentially useful for cancer chemotherapy

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REFERENCE
AUTHORS
                                          FEATURES
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                           Mueller-Schilling, M., Krammer, P. and Oren, M.
Rovel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
patent: DE 19847779-C 24 03-FEB-2000;
DEUTSCHES KREBSFORSCH (LE)
                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                               AX026112.1 GI:10187543
                                                                                                                                                                                                   Sequence 24 from Patent DE19847779. AX026112
                                                                                                                                                                                                                         AX026112
                                                                                                                                                                                                                                                                                                1 GGACAAGCCCTGACAAGCCA 20
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19947779-C 10 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DEUTSCHES KREBSFORSCH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                   7 a
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AX026120
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Direct Submission
Submitted (08-SEP-1998) Mueller M., Department of Internal Medicine
IV, University Hospital, Bergheimerstr. 58, Heidelberg, 69115,
                                                                                         p53 activates the CD95 (APO-1/Fas) gene in response to DNA damage J. Exp. Med. 188 (11), 2033-2045 (1998)
                                                                  Mueller, M.
                                                                                                                                      Mueller,M., Wilder,S., Bannasch,D., Israeli,D., Lehlbach,K., Li-Weber,M., Friedman,S.L., Galle,P.R., Stremmel,W., Oren,M. and
                                                                                                                                                                                                                                                                                                                                                            160 GGACAAGCCCTGACAAGCCA 179
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                               CD95 gene; enhancer
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                                                                                                                                                                                                                                                                      Homo sapiens DNA for enhancer of CD95 gene, partial.
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                                                                          (bases 1 to 266)
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/db_xref="taxon:9606"
72 c 110 g
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/db_xref="taxon:9606"
7 c 5 g
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tive 0; Mismatch
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Sequence 2 from Patent DE19847779.
AX026090
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 3 from Patent DE19847779.
AXO26091
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Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy patent: DE 19847779-C 3 03-FEB-2000;
                                                                                                 Homo sapiens
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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159. .178
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72 c 110 g
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181 c 216 g
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                         3212 bp
Sequence 1 from Patent DE19847779.
AX026089
                                                 Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 1 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol type="genomic DNA"
/db xref="taxon:9606"
/db 7676 c 657 g 761
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100.0%; Pred. No.
/mol_type="genomic
 /organism="Homo sapiens"
/mol_type="genomic DNA"
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100.0%; Pred. No.
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AL Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14161146.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

regions were either double-stranded or sequenced with an alternate
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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t: WO 03008583-A 1262 30-JAN-2003;
s Discovery (US)
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/db_xref="taxon:9606"
8836 c 9010 g 1
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784 c 809 g
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100.0%; Pred. No. 14;
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                                                                                                                             Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 6.03-FEB-2000;
                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 6 from Patent DE19847779.
AX026094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Sequence from AC015461 sequenced by WIBR."
105973. 105989 /note="Sequence confirmed by AC015461 sequenced by WIBR."
55669 a 36398 c 36888 g 58358 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
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                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100119: .100156
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/chromosome="10"
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sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 26% of reads
Dye-terminator Big Dye; 73% of reads
Oye-terminator Big
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19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (18-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerequest@sanger.ac.uk requests: clonerequest@sanger.ac.uk on Oct 21, 2001 this sequence version replaced gi:12539659.
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code:
                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence this soon as it is available and the accession number will be preserved.
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51755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               project Information
                                                                                                                                                                                                                                     12019: contig of 12019 bp in length
12119: gap of 100 bp
32657: contig of 20538 bp in length
32757: gap of 100 bp
32757: gap of 3348 bp in length
36105: contig of 3348 bp in length
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                                                                                                                                                                                                                       gap of 100 bp
                                                                                                                                gap of 100 bp
contig of 10485 bp in length
gap of 100 bp
                                          contig of 10643 bp in length
gap of 100 bp
contig of 11098 bp in length
gap of 100 bp
contig of 9582 bp in length gap of 100 bp
                                                                                                                                                                                                   contig of 4864 bp in length
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101274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment:00380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="RPCI-5"
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fragment_chain:1"
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83378. .
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ragment_chain:1"
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fragment_chain:1"
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ragment_chain:1"
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ragment_chain:1"
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158200: gap of 100 bp
161982: contig of 3782 bp in length
162082: gap of 100 bp
167412: contig of 5330 bp in length.
                                                                                                                                               /note="assembly_fragment:00350
fragment_chain:3"
109821. .114256
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:01125fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:00248
?ragment_chain:2"
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28350: contig of 8623 bp in length
                                                                                                                                                                                                                  /note="assembly fragment:01704 fragment_chain:3" 103521 109720
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                                                                               /note="assembly_fragment:01435
fragment_chain:3"
114357...119627
                                                                                                                                                                                                                                                                                    fragment_chain:
101274. .103420
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                                                                                                                                                                                                                                                                                                                     98946. .101173
/note="assembly_fragment:01201
fragment_chain:2"
                                                      /note="assembly_fragment:00291
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5: gap of 100 bp
3: contig of 2228 bp in length
3: gap of 100 bp
0: contig of 2147 bp in length
0: contig of 6200 bp in length
0: gap of 100 bp
6: contig of 6436 bp in length
6: gap of 100 bp
6: contig of 4436 bp in length
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REFERENCE
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ORIGIN
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequence submission with sequence was finished as follows unless otherwise noted: all sol); an attempt was made to resolve all sequenced with a alternate as compression and repeats; all regions were either double-stranded or sequenced with an alternate as compressions and repeats; all regions were covered by high quality deal sequencing problems, such assembly was confirmed by restriction of the cover do the rare plasmid subclone or more than one M13 subclone; and the occasion of the clone being a yAC.

numbers given in the feature table with their source databases:
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                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-APR 2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
On Nov 27, 2002 this sequence version replaced gi:24394955.
Sequence from the Mouse Genome Sequencin replaced gi:24394955.
shotgun may have been used to confirm this sequence whole genome from the whole genome shotgun and the sequence data a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                      Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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192657 bp DNA linear ROD 17-APR-2003
Mouse DNA sequence from clone RP23-144K18 on chromosome 4, complete
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41496 a 41224 c 42341 g 40447 t 1
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162083. .167412
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fragment_chain:5"
140284. 147703
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fragment chain:4"
128451 140183
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58201. .161982
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95.0%; Pred. No. 7(
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* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 190946 bases at least Q40
Consensus quality: 191521 bases at least Q20
Consensus quality: 191667 bases at least Q20
Insert size: 192452; sum-of-contigs
Insert size: 197663; 4.4% error; agarose-fp
Coverage: 8.09x in Q20 bases; sum-of-contigs Quality
Coverage: 8.09x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156517 GGĀCĀĀGCCAGĀCĀĀGCCĀ 156536
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-ARR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 2, 2003 this sequence version replaced gi:29134752.
Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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For further details see http://www.chori.org/bacpac/home.htm
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Search completed: August 1, 2003, 17:32:49 Job time: 83.1573 secs

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                                               Contect: Robert Strausberg, Ph.D.

Contect: Robert Strausberg, Ph.D.

Contect: Robert Strausberg, Ph.D.

Contect: Robert Strausberg, Inc.

Tissue Procurement: Life Technologies, Inc.

Tissue Procurement: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be Clone distribution. MGC clone distribution information can be conditionally in the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 554.r For
more information about this cluster, sequence cluster 554.r For
http://www.genoscope.cns.fr/
Cgi-bin/Cluster.cgi?seq=CSODE002DE09QP1&cluster=5554.r For
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE002DG09QP1.
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Contact: Genoscope
Genoscope - Centre National de Sequencage
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5-PRIME, mRNA sequence.
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/tissue type="placeNTA"
/clone Tib="Homo sapiens PLACENTA"
/note="Tvector: pcMvSpORT 6; 1st strand cDNA was primed double-strand cDNA was digested with Not I and cloned, the Not I and ECORV sites of the pcMvSpORT 6 vector.

Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B., Gruber,C., Jessee,J. and Polayes,D.
length cDNA libraries and normalization
                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref."taxon:9606"
/clone="CS0DE002YN18"
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//Lord lib="NIIH M
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/moi_type="mRNA"
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/clone="IMAGE:5189752"
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W45225
zc23c09.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Consortium (Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAND TOW: 1 Column: 21

Uich mality://mage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                          280 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                              ilarity 100.0%; Score 20; DE Conservative 0; Mismatch 20;
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AGENCOURT 6763280 NIH MGC_118 Homo sapiens cDNA clone IMAGE:5756324
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                                                                                                                                                                                                                           /clone_lib="NIH MCC_118"
/note="Wector: pCWV-SPORT6; Site_1: Not1; Site_2: EcoRV non-activated adult donors. Library is oligo-dT primed cloning). Average insert size 1.7 kb, insert size range full-length clones and was constructed do for full-length clones and was constructed by C. Gruber this is a NIH MGC Library."

[Invitrogen]. Research Genetics tracking code 027. Note: 80 a 263 c 333 g 212 t 1 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5756324"
/tissue_type="leukocyte"
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tive 0; Mismatches
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman Hillier, L., Clark, N., Dubuque, T., Eennon, G., Marra, M., Parsons, J., M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., R., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R., R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                        265 GACAAGCCCTGACAAGCC 282
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Seq primer: mob.REGA+ET
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                                                                                                                           TgESTzya24g01.y1 TgVEG118 Tachyzoite cDNA Library Toxoplamma gondii cDNA clone TgESTzya24g01.y1 5' similar to TR.063030 Q63030 RAT ALPHA-SMOOTH MUSCLE ACTIN MRNA FRAGMENT ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
                                                                                             BG659530.1 GI:13801991
                                                       Toxoplasma gondii
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/lab host="DH10B (ampicillin resistant)"
/lab host="DH10B (ampicillin resistant)"
/clone_lib="searces senescent_fibroblasts_NbHSF"
/clone_lib="searces senescent_fibroblasts_modified
/note="vector: pT7T3D (Pharmacia) with a modified
/note="vector: pT7T3D (Pharmacia) with a Not I; Site_2: Eco RI
polylinker V_TYPE: phagemid; Site_1: Not I; Oligo(dT)
; lst strand_cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."
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/db xref="taxon:9606"
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100.0%; Pred. No. 3.4e+02;
zive 0; Mismatches 0;
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Fax: 314 286 1810
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BU142933.1
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                                      12445392
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Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajloka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylle, T., Dante, M., Marra, M., Hiller, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter Hillier, L., Kucaba, T., Tranklin, C., Tsagareishvili, R., Ronko, I., Kennedy, B., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact David Sibley (toxoest@borcim.wustl.edu) for further (contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seq primer: -40RP from Gibco Seq primer: -40RP from Gibco High quality sequence stop: 371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4444 Forest Park Parkway, Box 8501,
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxoplasma EST Project
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Archosauria; Alus.

Phasianinae; Gallus.

1 (bases 1 to 753)

1 (bases 1 to 753)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J., A. Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (chicken)
Gallus gallus
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/clone lib="TgVEG118 Tachyzoite cDNA Library"
/note="Twector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI
/note="Twector: pBluescript SK; Site 1: EcoRI; Robert
; This library was constructed by Keliang Tang, Robert
; This library was constructed by Keliang Tang, Robert
; Cole, and L. David Sibley at Washington University. CDNAs
Cole, and L. David Sibley at Washington University. CDNAs
cole, and L. David Sibley at Washington University. CDNAs

size-selected and directionally cloned into the Uni-ZAP XR
size-selected and directionally cloned into the Uni-ZAP XR
lambda vector (Stratagene). The primary library was mass
lambda vec
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nes 0; Indels
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                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Seq primer: CACACAGGAAACAGCTATGACC
             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0197 row: J column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 GGÁCAAGCCTGÁCAAGC 179
                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 619)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.; Islam, H., Longacre, S., Mahmoud, M., Weenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                             prasmid
                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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A2939002
A2939002
A290197718R Mouse 10kb plasmid UUGC2M library Mus musculus clone UUGC2M0197718 R, genomic survey sequence.
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Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simon Hubbard
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                                                                                                                                                                                                                     whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="CSEQCHL25"
/note="Organ: brain; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: Not1; Modification of pBluescript II KS(+)
Istratagenel vector to accommodate cDNA produced with the cloned cDNA libraries from messenger RNA for improved 3', end DNA sequencing by Glenm FW, et al. U.S. Patent # 6,387
Ligate in double stranded adaptor containing BsgI and [5'aattcttttttctggatcggggctgcacgc]"
BamHI sites [5'ggccggtgcacgcggggtgcacaaaaaaag]
[5'aattctttttttttggatcggggtgcacgcg]"
                                                                                                                  USA
                                                                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST11919"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%; Score 18; DB 13; Length 753; 100.0%; Pred. No. 3.9e+02;
                             Std Error: 0.00
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                                                                                                                                      COMMENT
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AUTHORS
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BASE COUNT
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     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errc
Plate: 0249 row: M column: 17
                                                                                                                                                                             University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 684)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., Mand Wright, D., Weiss, R.
                                                                                                                                                                                                                                   Contact: Robert B.
                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                       USA
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                                                                                                                         Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA polymuleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC2M library"/note="Vector: PMP42nv; Purified genomic DNA from M. musculus C578L/6J (female) was obtained from the Jackson rahoratory Mouse num Bonouver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                             Weiss
column: 17
                  Std Error: 0.00
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UUGC1M library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GACAAGCCCTGACAAGCCA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Danio rerio genomic clone DKEY-269M11, genomic survey sequence.

BX220214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 689)
Humphray, S.J., Huckle, E. and Durham, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX220214.1 GI:28052100
                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was generated from the SP6 end of BAC 269M11. 269M11 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei, Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campus, Hinxton, Cambridgeshire, Campus, Hinxton, Cambridgeshire, Cambridgeshire, Cambridgeshire, Campus, Hinxton, Cambridgeshire, Campus, Hinxton, Campus, Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                         Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/) was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt ends in high mollar excess. The ligated to the blunt ends in high mollar excess. The adaptored DNA was purified and size-selected for a 9.5 to adaptored DNA was preparative agarose gel 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNDA2 (gi|4732114|gb|AF129072.1), a copy-number of pNDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid(R1. The vector was ligated with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 a
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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/tissue_type="Testis"
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                 Clone="DKEY-269M11"
                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                            organism="Danio rerio"
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94.7%;
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BX179961/c
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VERSION
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                                                                                                                                                                                                                 255 GGACAAGCCCAGACAAGCC 237
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miao, G., Caraner, N. and had
DuPont Wheat cDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                1 GGACAAGCCCTGACAAGCC 19
                                                                                                                                                                                                                                                                                 18;
                                                                                                 Danio rerio genomic clone DKEY-183M20, genomic survey sequence.
BX179961
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                                                                                                                                                                                                                                                                                                 Similarity
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                Danio rerio (zebrafish)
                                                                                 BX179961.1 GI:28011764
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144 c 144 g 221 t
                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum L.) root; 7 day old seedling, light grown"
188 c 131 g 156 t 27 others
                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4565"
/clone="wrl.pk0046.e7"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Triticum aestivum"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:25160333
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                                                                                                                                                                                                                                                                                                   87.0%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type="mRNA"
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Pred. No. 7.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                   Score 17.4; DB 14;
Pred. No. 7.4e+02;
                                                                                                                                        DNA
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                                                                                                                                             GSS 28-JAN-2003
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FEATURES
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TITLE
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                                                                                                                                                                                                                                                                               Seq primer:
                                                                                                                                                                                                                                                                                                      Clone information and library can be obtained from Jim Ajioka
                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Parasite Genome Analysis
Cambridge University
Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.
                                                                                                                                                                                                                                                                                                jwa@mole.bio.cam.ac.uk
                                                                                                                                                                                                                                                                                                                                                             Fax: 01223333923
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Ajioka JW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wan,K.-L., Blackwell,J.M. and Ajioka,J.W.
Toxoplasma gondii expressed sequence tags: insight into tachyzoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GACAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sarcocystidae; Toxoplasma.

1 (bases 1 to 331)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F62311.1 GI:665753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 183M20. 183M20 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 745)
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                                                                                                                                                                                                                                                                                                                                 jajioka@hgmp.mrc.ac.uk
/lab_host="XLI-Blue MRF/"
/clone lib="TgRH Tachyzoite cDNA"
/clone lib="TgRH Tachyzoite cDNA"
/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
/noxoplasma RH strain tachyzoites were grown in human
foreskin fibroblast cultures in vitro. The library was
constructed by K.L. Wan, Cambridge University. cDNAs we
                                                                                                                                    clone="tgb008"
                                                                                                                                                       db_xref="taxon:5811"
                                                                                                                                                                                               /mol_type="mRNA"
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                strain="RH"
                                                                                                                                                                                                              'organism="Toxoplasma gondii"
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/tissue_type="Testis"
/note="vector pIndigoBAC-536"
150 c 151 g 235 t
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/db_xref="taxon:7955"
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94.7%;
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Pred. No. 7.6e+02;
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          cDNAs were
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 10000 Std Error: (Plate: 0018 row: K column: 23 Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 429)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                     /lab host="B. Coli strain XL10-Gold, Tl-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: pMp42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                    Clone="UUGC2M0018K23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                     sex="Male"
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3', mRNA sequence.
AA195416
AA195416.1 GI:1785109
EST.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
,T., Waterston,R. and Wilson,R.
Washu_Merck EST Project 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1020 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
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                                                            /clone_lib="Soares NhHMPu S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I M.A.G.B. clones 260232-265223,
340488-345479, and 484488-489479."

11 a 110 c 167 g 141 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="GDB:5427547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"

mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     one="IMAGE:665515"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xref="taxon:9606"
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Pred. No. 9.6e+02;
Score 16.8;
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  Length 531;
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Search completed: August Job time : 72.4754 secs

2003, 20:42:58

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AW131236/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW131236 592 bp mRNA linear EST 27-OCT-19: xf60c04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622438 3' similar to SW:TF1B_HUMAN Q13263 TRANSCRIPTION INTERMEDIARY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 592)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-BETA ;, mRNA sequence.
AW131236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                      Similarity
GGACAAGCTCTCACAAGCCA 571
                                      GGACAAGCCCTGACAAGCCA 20
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                                                                                                                                                                                                                       /clone_lib="NCI_CGAP_Gas4"
//note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT.
Sycarage insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                     /tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                        11549-011"
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                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:2622438"
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                                                                                                 84.0%;
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AAK74243 ACA01448 AAK74241

> Propionibacterium Human immune/haema

glutamicum deri glutamicum deri

Human

immune/haema immune/haema

Human immune/haema Neisseria gonorrho Neisseria gonorrhe Neisseria mening Neisseria meningit

AAK95694 AAK97187

ABX58612 ABN68645

> Streptococcus poly Human musculoskele Human neuregulin-1 Human neuregulin-1 Human neuregulin g Human neuregulin g Bovine EST associa C glutamicum codin

Human gene express CDNA encoding nove

cDNA encoding nove Human musculoskele cDNA sequence

Human musculoskele

cDNA encoding nove

ABX60548

Human secreted pro Aspergillus fumiga

Aspergillus fumiga

ABT19714

ALIGNMENTS

ABN85735 AAH68534

Human gene express Human immune/haema propionibacterium 88421nt genomic

AAS59585 AAS59679

AAK81660

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                   16.4
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1: /SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn.emb1/NA1983.DAT:*
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2003 Compug
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                                                                AAZ88700
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                                                                                                                           Description
                                                            Murine gene trappe
Secreted protein g
Human immune/haema
                                   Secreted protein 9
Bovine EST associa
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          N. gonorrhoeae nuc
                        Human GDP-mannose
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                                                                                                                                                                                                                                                                        p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                 protein_bind
                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                               cancer chemotherapy; ss.
                                                                                                                                                 DE19847779-C1.
                                                                                                                        03-FEB-2000.
                    Krammer P, Mueller-Schilling M, Oren M;
                                                                       16-OCT-1998;
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The present invention relates to novel murine cDNAs produced using gene trap technology. The OMNIBANK gene trapped sequences (GTSs) are individually identified novel genes, and are useful in functional genomic analysis, in the discovery and development of new therapeutic and diagnostic agents, for gene discovery, for diagnostic gene expression analysis, for cross species hybridiaation analysis, and for genetic manipulations such as antisense inhibition or gene targeting.
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                                                                                                                              Claim 2; SEQ ID NO 1101; 29pp; English.
                                                                                                                                                 functional genomic analysis, in the development of new ther diagnostic agents, for diagnostic gene expression analysis genetic manipulations
                                                                                                                                                                        New murine polynucleotides comprising gene trapped sequences, useful in functional genomic analysis, in the development of new therapeutic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                    Friedrich G,
                                                                                                                                                                                                                                        WPI; 2003-288124/28.
                                                                                                                                                                                                                                                                                                                                                         01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2000; 2000US-0728444.
                                                                                                                                                                                                                                                                                               (SAND/) SANDS A T.
                                                                                                                                                                                                                                                                                                                         (FRIE/) FRIEDRICH G.
                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002161207-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine; mouse; gene trap technology; gene trapped sequence; GTS; gene identification; functional genomic analysis; gene discovery; gene expression analysis; cross species hybridisation analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense inhibition; gene targeting; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine gene trapped sequence (GTS) SEQ ID No 1101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABX91757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABX91757 standard; cDNA; 516 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for canner chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 4; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy -
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                                                                                                                                                                                                                                                                                                             ZAMBROWICZ B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACAAGCCCTGACAAGCCA 179
                                                                                                                                                                                                                                                            Zambrowicz B, Sands AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                     99US-168360P
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                                                                                                                                                                                                                               New human secreted proteins and nucleic acids, useful for detecting or treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia -
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                                                                                                                                                                                                       Disclosure; Page 2282-2284; 2474pp; English.
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                                                                                                                                                                                                                                                                                                                       WPI; 2003-040578/03.
                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001; 2001US-278650P.
12-SEP-2001; 2001US-0950082.
12-SEP-2001; 2001US-0950083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002; 2002WO-US09370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; cancer; tumour; hyperproliferative disorder; autoimmune disorder; inflammation; angiogenic diseases; AIDS; acquired immunodeficiency syndrome; hepatitts; anaemia; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV; antianaemic; vulnerary; chromosome 15q24-25; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277013-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein gene 346 genomic fragment HTOHO21, SEQ ID NO:1700.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ74553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ74553 standard; DNA; 8243 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The polynucleotides of the invention are also useful for isolating cDNAs, genomic clones or full-length genes/polynucleotides, or their homologues, heterologues, paralogues or orthologues, that are capable of hybridising to one or more of the new murine polynucleotide sequences. The polynucleotides are also useful for identifying the coding regions of the murine genome, and as hybridisation probes. ABX90657-ABX91862 represent the murine GTSs of the invention. Where the sequence data for this patent did not form part of the printed uspro web site at seqdata.uspto.gov/psipsDIDEntry.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 516 BP; 163 A; 90 C; 118 G; 140 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 GACAAGCGCTGACAAGCC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GAÇAAGCCCTGAÇAAGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%;
94.4%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing or treating cancers or other and hyperproliferative disorders. Additionally, the secreted proteins and hyperproliferative disorders. Additionally, the secreted proteins and their nucleic acids may also be used in the treatment of autoimmune their nucleic acids may also be used in the treatment of autoimmune disorders, diseases involving angiogenesis, AIDS disorders inflammatory disorders, diseases involving angiogenesis, AIDS disorders, diseases involving and oppose wound healing. Nucleic acids of the invention may be used for chromosome wound healing. Nucleic acids of the invention may be used for chromosome mapping, in gene therapy, for identifying identification, chromosome mapping, in gene therapy, for identifying and individuals from minute biological samples, as hybridisation probes, and individuals from minute biological samples, as hybridisation probes, and individuals from minute biological samples, as hybridisation probes, and individuals from minute biological samples, as hybridisation probes, and individuals from minute biological samples, as hybridisation probes, and individuals from minute biological samples and individuals from minute biological samples to the properties of the secreted protein genomic fragment referred to in the disclosure of the spectrated protein genomic fragment referred to in the disclosure of the spectrated protein genomic fragment referred to in the disclosure of the spectrated protein genomic fragment referred to in the disclosure of the spectrated protein genomic fragment referred to in the disclosure of the spectrated protein genomic fragment referred to in the disclosure of the spectrated protein genomic fragment referred to in the disclosure of the spectrated protein generated protein genomic fragment referred to in the disclosure of the spectrated protein generated protein generated protein generated protein generated protein generated protein generated protein 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35824.
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                                           14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
02-OCT-2000;
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13-OCT-2000;
13-OCT-2000;
20-OCT-2000;
20-OC
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27-SEP-2000;
27-SEP-2000;
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21-SEP-2000;
25-SEP-2000;
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01-NOV-2000;
08-NOV-2000;
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2000US-0225759.
2000US-0226279.
2000US-0226681.
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2000US-0227182.
2000US-0227009.
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2000US-0231968.
2000US-0232397.
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2000US-0229287.
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2000US-0234273.
2000US-0234274.
2000US-0234997.
2000US-0234998.
2000US-0235484.
2000US-0235484.
2000US-0235834.
2000US-0235834.
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2000US-0233063.
2000US-0233064.
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2000US-0236367.

2000US-0236369.

2000US-0236370.

2000US-0236370.

2000US-0236373.

2000US-0236073.

2000US-0237039.

2000US-0237039.

2000US-0237049.
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2000US-0232080.
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2000US-0232399.
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2000US-0246526.
2000US-0246527.
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2000US-0239937.
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2000US-0241808.
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2000US-0246474.
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2000US-0246523.
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2000US-0246532.
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WPI; 2001-483426/52.
                                                                                        08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                  08-NOV-2000; 2000US-0246610.
                                                                          Barash SC, Ruben SM;
                                                                                      2001US-0259678.
                                                                                                                      2000US-0250160.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 35824; 3071pp + Sequence Listing; English.

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC the nucleotides may be used to produce the secreted (I), by inserting CC protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC expresent human immune/haematopoietic antigen genomic concers from the present invention. AAK4942 to AAK54950 and AAM82169 XXX

Query Match Best Local ! Sequence 12710 BP; 3496 A; 2567 C; 2575 G; 4072 T; 0 other;

Maţches Similarity Conservative 82.0%; Score 16.4; DB 22; Length 12710; 94.4%; Pred. No. 2e+02; 0; Mismatches 2e+02; 1;

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2 GACAAGCCCTGACAAGCC 19
            Indels
         0; Gaps
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RESULT 5
ABZ74552
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12-SEP-2001; 2001US-0950082.
12-SEP-2001; 2001US-0950083.
                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                              26-MAR-2002; 2002WO-US09370
                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV; antianaemic; vulnerary; chromosome 15q24-25; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; cancer; tumour; hyperproliferative disorder; autoimmune disorder; inflammation; anglogenic diseases; AIDS; acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing; drug screening; chromosome identification; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein gene 346 genomic fragment HTOHO21, SEQ ID NO:1699.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ74552 standard; DNA; 12710 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 GACAAGCCCTGAGAAGCC 79
                                                                                                                                                                                                                                                              Ruben SM;
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New human secreted proteins and nucleic acids, useful for detecting or treating cancer or other hyperproliferative disorders, autoimmune inflammatory disorders, HIV disease, hepatitis or anemia -

Disclosure; Page 2278-2281; 2474pp; English.

CC protein genes, and ABB00947-ABB01363 represent the proteins they encode.
CC ABZ73698-ABZ74687 represent human secreted proteins they encode.
CC invention also encompasses antibodies specific for the secreted proteins. The
CC vectors and host cells comprising a nucleic acid of the invention. The
CC secreted proteins are thought to be involved in biological activities
CC associated with cellular signalling, cellular signation, cellular differentiation, cell
CC secreted proteins, nucleic acids encoding them, antibodies or antibody
CC fragments specific for the secreted proteins, and neurotransmitter activity. The
CC fragments specific for the secreted proteins, and modulators of protein
CC fragments specific for the secreted proteins, and modulators of protein
CC fragments specific for the secreted proteins, and modulators of protein
CC fragments specific for the secreted proteins or other
CC their nucleic acids may also be used in the treatment of autoimmune
CC disorders, inflammatory disorders, diseases involving angiogenesis, AIDS
CC (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote
CC undividuals from minute biological samples, as hybridisation probes, and
CC as molecular weight markers. The present sequence represents a human
CC invention. ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted protein genes, and ABP00947-ABP01363 represent the proteins they encode.

Sequence 12710 BP; 4072 A; 2575 C; 2567 G; 3496 T; 0 other;

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Best
                                  Query Match
                      Local Similarity
              17;
            Conservative
  82.0%; Score 16.4; DB 25;
94.4%; Pred. No. 2e+02;
". Mismatches 1;
                  DB 25; Length 12710;
   Indels
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cc lactation or muscle and fat deposition (designated LMPD) derived cc from cattle, and the LMPD nucleic acid can specifically hybridise to a cc from cattle, and the LMPD nucleic acid can specifically hybridise to a cc second nucleic acid molecule comprising any of 5912 nucleotide cc also included are; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic acid linked to a promoter and a 3 non-cc translated sequence that functions in the cell to cause termination of translated sequence that functions in the cell to cause termination of compressing an LMPD nucleic acid linked to a promoter and a 3 end cranscription and addition of polyademylated ribonucleotides to a 3 end cranscription and addition of polyademylated ribonucleotides to a 3 end cranscription and addition of polyademylated ribonucleotides to a 3 end cranscription and addition of polyademylated ribonucleotides to a 3 end cranscription and addition of polyademylated ribonucleotides to a 3 end cranscription and addition of polyademylated ribonucleotides to a 3 end cranscription of the molecule; and (2) determining a level or pattern of a nucleic acid (comprising any of the 5912 nucleic acid melecule complement or fragment) with a complement ary nucleic acid melecule the complement ary nucleic acid permits the complement ary nucleic acid melecule. The complement ary nucleic acid where the detection of the molecule. The LMPD nucleic acid is used for determining a level or pattern of the molecule. The LMPD nucleic acid is used for determining a level or pattern of the molecule. The present sequence is one of the 5912 bowline constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression, or for genetically constructs for use in cattle gene expression with the specification but the construct of the molecule acids.

CC LMPD EST (expressed sequence was not shown in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX52814 standard; cDNA; 433 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine; 88; EST; expressed sequence tag; lactation; LMFD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos Taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002137160-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       muscle deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2001; 2001US-0983965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1998;
15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Byatt JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              purified nucleic acid molecules, useful for genome mapping, identification and analysis, cattle breeding or preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-102386/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BYAT/) BYATT J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID No 2743; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructs for cattle gene expression and genetically improved cattle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACAAGCCCTGAGAAGCC 12632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mathialagan N, Tao N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-113678P.
99US-0465231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Warren WC;
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RESULT 7
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                                The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying CC GM4,6D inhibitors are useful for reducing inflammation (CC GM4,6D inhibitors are useful for reducing inflammation of gladest and for treating or ameliorating diseases affected by the CC by the level of cellular fucosylation or diseases include arthritis. CC fucosylation of glycoconjugates These diseases include arthritis. CC infection. The GM4,6D peptide or a polymucleotide encoding it is also CC constitution. The GM4,6D peptide or a polymucleotide encoding it is also CC useful for manufacturing complex carbohydrates and as targets for CC useful for manufacturing complex carbohydrates and as targets in the CC screening small molecule antagonists of the activity of the enzyme. The CC screening small molecule antagonists of the activity defects in the CC screening small molecule arthrighy. Sequences polymucleotide is useful in developing an assay for defects in the CC screening and ABX17947-ABX3716 represent DNA molecules encoding CC ABX17942-ABX17944 and ABX17947-ABX3716 represent DNA molecules encoding CC Note: The sequence data for this patent did not form part of the printed CC specification but was obtained in electronic format directly from USPTO creaming the property of the complex contains the sequence data for this patent did not form part of the printed CC are served to the contained in electronic format directly from USPTO contained the contained in electronic format directly from USPTO contained the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation; cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective; antiinflammatory; antiarthritic; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX27459 standard; cDNA; 165 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #9516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX27459;
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03-DEC-1997;
09-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for peptide, for manufacturing complex carbohydrates, or transplant screening GM4,6D antagonists for treating e.g. arthritis, or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 9518; 6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rejection
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                     seqdata.uspto.gov/sequence.html.
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97US-0984246.
98US-0149674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kumar R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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RESULT 9
AAZ11974/c
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Best Local
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                          08-OCT-1999 (first entry)
                                                   AAZ11974;
                                                               AAZ11974 standard; DNA; 273 BP.
                                                                                                                                                                                                              The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention.
                                                                                                                                                                                                 Sequence 261 BP; 53 A; 71 C; 65 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                               New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection
                                                                                                                                                                                                                                                                                                                     Disclosure; Page 746; 815pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                               Fontana MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2001; 2001GB-0003424.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2002; 2002WO-IB02069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200279243-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria gonorrhoeae.
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; infection; vaccine; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N. gonorrhoeae nucleotide sequence SEQ ID 7651.
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                                                                                                                    153 GACAAGCCTTGCCAAGCCA 171
                                                                                                                                                                   17;
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                                                                                                                                         2 GACAAGCCCTGACAAGCCA 20
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 GGACAAGCTCGGACAAGCC 149
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                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                               79.0%; Score 15.8; DB 25; Length 261; 89.5%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V, Monaci E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.0%; Score 15.8; DB 25; Length 165; 89.5%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.5%;
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11-NOV-1999.

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RESULT 10
AAZ53178
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                                     Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                     Neisseria meningitidis.
                                                                           Neisseria meningitidis ORF 091 partial DNA sequence SEQ ID NO:307.
                                                                                                                         21-MAR-2000
                                                                                                                                                                  AAZ53178 standard; DNA; 288 BP
                                                                                                                                                   AAZ53178;
                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFS) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful
                                                                                                                                                                                                                                                                                                                      Sequence 273 BP; 75 A; 67 C; 83 G; 48 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 61; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY38501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-327407/27.
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06-NOV-1997;
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18-NOV-1997;
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                                                                                                                                                                                                                                                                                              ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis strain A complete ORF37 sequence.
                                                                                                                                                                                                                             217 GACAAGCCTTGCCAAGCCA 199
                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                      2 GACAAGCCCTGACAAGCCA 20
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98GB-0000759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97GB-0024386.
97GB-0025158.
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                                                                                                                                                                                                                                                                                      79.0%; Score 15.8;
89.5%; Pred. No. 2.
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                                                                                                                                                                                                                                                                                      2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scarlato V;
                                                                                                                                                                                                                                                                                             Length 273;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. genorrheae polymucleotides and polypeptides. AAZ54576 to AAZ54576 and AAZ54616 to AAZ5437 represent primers used in the exemplification of the present invention. The polypeptides, the polymucleotides, antibodies and compositions of polypeptides of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the immunogenic compositions for treating or preventing infection due to manufacture of medicaments for treating or preventing infection due to presence of Neisseria bacteria, or to raise antibodies. They may also presence of Neisseria bacteria, or antagonists, which may themselves be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C,
Petersen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 287; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY74416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 288 BP; 57 A; 73 C; 74 G; 84 T; 0 other;
                                                                                                                                                                                                                                                            AAZ53176 standard; DNA; 309 BP
                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                           Neisseria gonorrheae ORF 091 partial DNA sequence SEQ ID NO:303.
                                                                                                                                                                                                      21-MAR-2000 (first entry)
                                                                                                                      antibacterial; gene therapy; ds.
                                                                                            Neisseria gonorrheae
             30-APR-1999;
                                                                    WO9957280-A2
                                        11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-062150/05.
                                                                                                                                                                                                                                                                                                                                198 GACAAGCCTTGCCAAGCCA 216
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                                                                                                                                                                                                                                                                                                                                                          2 GACAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US09346.
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                 99WO-US09346.
                                                                                                                                                                                                                                                                                                                                                                                                         79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8; DB 21; Length 288; Pred. No. 2.4e+02;
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, Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scalato E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scarselli M;
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RESULT 12
AAZ11975/
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                                       01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent protes used in the exemplification of the present invention. The polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to manufacture of medicaments for treating or preventing infection due to manufacture of medicaments for treating or preventing infection due to presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves be used to screen for agonists or antagonists, which may themselves are use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 287; 1453pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY74414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-)
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                                                                                                                                                                                                                                                                                           AAZ11975 standard; DNA; 381 BP
                                                                                                                                                                                                                                                                    AAZ11975;
01-SEP-1998;
06-NOV-1997;
14-NOV-1997;
                                                                                                                                                                Neisseria meningitidis, Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.
                                                                                                                                                                                                         Neisseria gonorrhoeae complete ORF37 sequence.
                                                                                                                                                                                                                                       08-OCT-1999
                                                                                                                                      Neisseria gonorrhoeae.
                                                                                                              WO9924578-A2
                                                         09-OCT-1998;
                                                                                   20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                             2 GACAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0083758.
98US-0094869.
98US-0098994.
98US-0099062.
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98US-0103796.
99US-0121528.
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                                                                                                                                                                                                                                          (first entry)
      97GB-0023516.
97GB-0024190
                                                            98WO-IB01665.
                               98GB-0019016.
                                                                                                                                                                                                                                                                                                                                                                                                                                           79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8; DB 21; pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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, Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani V, Mora...
Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 309;
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AAK58992
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                     31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0186364.
02-MAR-2000; 2000US-0186350.
16-MAR-2000; 2000US-0198174.
18-APR-2000; 2000US-0198123.
19-MAY-2000; 2000US-020515.
28-JUN-2000; 2000US-020467.
28-JUN-2000; 2000US-0214886.
07-JUL-2000; 2000US-021515.
07-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                 WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:4052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK58992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK58992 standard; cDNA; 409 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFS) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 381 BP; 106 A; 84 C; 114 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 61; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY38502.
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27-NOV-1997;
10-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 GACAAGCCTTGCCAAGCCA 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 89.5
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    therapy; vaccine; metastasis; ss.
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97GB-0025158.
97GB-0026147.
98GB-0000759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
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2000US-0229509

2000US-0230431

2000US-0230431

2000US-0231243

2000US-0231243

2000US-0231243

2000US-0231414

2000US-0231414

2000US-0231414

2000US-0231414

2000US-023408

2000US-023288

2000US-0232398

2000US-0232398

2000US-0232398

2000US-0232398

2000US-0232398

2000US-0232398

2000US-0232398

2000US-023398

2000US-023398
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2000US-0235836.
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2000US-0229343.
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2000US-0220964.
2000US-0224518.
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2000US-0225447.
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08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

2000US-0246474.

08-NOV-2000;

2000US-0246528.

2000US-0246609.

2000US-0246524. 2000US-0246525.

Indels

0

Gaps

0

2000US-0246523. 2000US-0246478.

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17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249215.
17-NOV-2000; 2000US-0249216.
AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For treatment of the used to treat disorders, associated with decreased example, they may be used to treat disorders, associated with instant's genome that affect the activity of (I) by expressing inactive proteins or to that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (b) inserting polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                    Claim 1; SEQ ID NO 4052; 3071pp + Sequence Listing; English.
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2000US-0246611.
2000US-0246613.
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2000US-0249245

2000US-0249264

2000US-0249265

2000US-0249297

2000US-0249297

2000US-0249299
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2000US-0249208.
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2000US-0251990.
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                                                                                                                                                                                                                                                                                                                                                              Ruben SM;
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AAK74242
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 409 BP; 93 A; 105 C; 96 G; 111 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK74242 standard; DNA; 749 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29054.
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-2000;
                                       14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
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2000US-0190076.
2000US-0198123.
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2000US-0215135.
2000US-0216647.
                                                                                                                                                                                                             2000US-0225214
2000US-0225266
2000US-0225267
                                             2000US-0225759.
2000US-0226279.
2000US-0226681.
2000US-0226868.
2000US-0226868.
2000US-0227182.
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2000US-0217487.
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2000US-0218290.
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                                                                                                                                               200005-0225757.
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89.5%; Pred. No. 2.
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17-NOV-2000; 01-DEC-2000; 01-DEC-2000; 05-DEC-2000;

Rosen CA, Barash SC,

P-PSDB; AAM86211.

2001-483426/52.

useful for preventing, metastasis -

17-NOV-2000;

17-NOV-2000;

17-NOV-2000;

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06-SEP-2000; 2000US-0231242; 08-SEP-2000; 2000US-0231242; 08-SEP-2000; 2000US-0231244; 08-SEP-2000; 2000US-0231244; 08-SEP-2000; 2000US-0231413; 08-SEP-2000; 2000US-0231414; 08-SEP-2000; 2000US-0232081; 14-SEP-2000; 2000US-0232081; 14-SEP-2000; 2000US-023298; 14-SEP-2000; 2000US-023298; 14-SEP-2000; 2000US-023298; 14-SEP-2000; 2000US-023298; 14-SEP-2000; 2000US-0232400; 14-SEP-2000; 2000US-0233063; 14-SEP-2000; 2000US-0233427; 25-SEP-2000; 2000US-023427; 25-SEP-2000; 2000US-023400; 2000US-023427; 25-SEP-2000; 2000US-023427; 25-SEP-2000; 2000U
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; 2000US-0249207.
; 2000US-0249208.
; 2000US-0249209.
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2000US-0246611.
2000US-0246613.
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2000US-0246525
2000US-0246525
2000US-0246527
2000US-0246528
2000US-0246528
2000US-0246509
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2000US-0241786

2000US-0241787

2000US-0241808

2000US-0241809

2000US-0241809

2000US-0244617

2000US-0246474

2000US-0246475

2000US-0246475

2000US-0246477

2000US-0246478
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2000US-0235834.
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                                                                                                                     AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC cancers and cancer metastases of haematopoietic-related diseases, especially to AAK67694 represent human immune/haematopoietic antigen genomic cc sequences from the present invention. AAK64962 to AAK64703 and AAM82169 cc represent sequences used in the exemplification of the present invention.
                                                                Matches
                                                                                            Query Match
                                                                                                      Sequence 749 BP; 201 A; 185 C; 137 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2000; 2000US-02519391

05-DEC-2000; 2000US-0251030

05-DEC-2000; 2000US-0251988

06-DEC-2000; 2000US-0254719

06-DEC-2000; 2000US-0251479

08-DEC-2000; 2000US-0251868

08-DEC-2000; 2000US-0251868

08-DEC-2000; 2000US-0251868
                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 29054; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483426/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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558 ĠĠÁĊÁTĠĆĊĊĠĠÁĊÁÁĠĊĊ 576
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               1 GGACAAGCCCTGACAAGCC 19
                                                        h 79.0%; Score 15.8; DB 22; Length 749; Similarity 89.5%; Pred. NO. 2.7e+02;
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2000US-0249265.
2000US-0249297.
2000US-0249297.
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2000US-0250391.
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                                                   Mismatches
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                                               Indels
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                                           Gaps
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RESULT 15 AAK74243

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2001WO-US01354.  2000US-0186628. 2000US-018664. 2000US-0198123. 2000US-0199076. 2000US-0209467. 2000US-0214886. 2000US-0216880. 2000US-0216880. 2000US-0216880. 2000US-0216880. 2000US-0216880. 2000US-0216880. 2000US-0225214 2000US-0225214 2000US-0225214 2000US-0225214 2000US-0225214 2000US-0225214 2000US-0225266. 2000US-0225266. 2000US-0225268. 2000US-0225268. 2000US-0225757. 2000US-0225758. 2000US-0225681. 2000US-0225681. 2000US-0225681. 2000US-0225681. 2000US-0225681. 2000US-0225681. 2000US-0225782. 2000US-0225783. 2000US-0225783. 2000US-0225783. 2000US-0225783. 2000US-0226681. 2000US-0229343. 2000US-0229343. 2000US-0229343. 2000US-0229343. 2000US-0229343. 2000US-0229343. 2000US-02231444. 2000US-0231243. 2000US-0231243. 2000US-0231244. 2000US-0231244. 2000US-0231244. 2000US-0232398.	•	haematopoietic; immune/haematopoietic ne therapy; vaccine; metastasis; ds.	(first entry) haematopoietic antigen genomic sequenc	rd; DNA; 749 BP.
		ic antigen; cancer;	ce SEQ ID NO:29055.	
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29-SEP-2000 29-SEP-2000 20-CCT-2000 02-CCT-2000 02-CCT-2000 02-CCT-2000 02-CCT-2000 20-CCT-2000 20-CCT	0000	28888		0000
2000US-0236373 2000US-0236802 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0239935 2000US-0241785 2000US-0241808 2000US-0241808 2000US-0241808 2000US-0241809 2000US-0246178 2000US-0246476 2000US-0246477 2000US-0246477 2000US-0246477 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246510 2000US-0246510 2000US-0246510 2000US-0246510 2000US-0246510 2000US-0246510 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249211 2000US-0249214 2000US-0249214 2000US-0249215 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249217 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249217 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249216 2000US-0249218	2000US-0236327. 2000US-0236367. 2000US-0236368. 2000US-0236369.	2000US-0234984. 2000US-0235484. 2000US-0235834. 2000US-0235836.	2000US-0233065. 2000US-0233265. 2000US-0234223. 2000US-0234274.	2000US-0232399. 2000US-0232400. 2000US-0232401. 2000US-0232463.

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Search completed: August 1, 2003, 13:55:14 Job time: 7.69868 secs
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
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06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251999.
08-DEC-2000; 2000US-0251999.
                                                                                                                                                                                                                        Sequence 749 BP; 201 A; 185 C; 137 G; 226 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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08-DEC-2000; 2000US-0251990.

11-DEC-2000; 2000US-0254097.

05-JAN-2001; 2001US-0259678.
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                                                                           558 GGACATGCCCGGACAAGCC 576
                                                                                                    1 GGACAAGCCCTGACAAGCC 19
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                                                                                                                                            79.0%; Score 15.8; DB 22; Length 749; 89.5%; Pred. No. 2.7e+02; ative 0; Mismatches 2; Indels 0;
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Maximum DB seq length: 2000000000
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US-10-027-632-87503
                                                   US-09-728-444-1101
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Sequence
Sequence
                                                                                                                                                                                                                                                           Sequence 5,
                                                                       Sequence 7, Appli
Sequence 9, Appli
Sequence 174763,
         Sequence 1101, Ap
Sequence 2743, Ap
Sequence 9518, Ap
Sequence 87503, A
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10, Appl
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10 m	Sequence 1882, Ap	1073 AF	1, 2	۲	ω	52		102	Sequence 102861,	Sequence 12//34/	Sequence 12//33,			0 0	500	Sequence zouro	Sequence 455, APP	Sequence 1007 Tr	Sequence 455, APP	, ,	Sequence 1, April	٠,	Sequence 6, Appli	, 1-	Sequence 316681,

## ALIGNMENTS

RESULT 1 US-09-834-291-5

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APPLICANT: Oren, Moshe
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR APPLICATION UNMERE: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; sequence 5, Application US/09834291
; patent No. US20020042064A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           US-09-834-291-5
              US-09-834-291-10

; Sequence 10, Application US/09834291

; Patent No. US20020042064A1

; GENERAL INFORMATION:
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LENGTH: 20
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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Best Local S
                                                                                                                                                                                                                                  Matches
APPLICANT: Krammer, Peter
                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                       ocal Similarity
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APPLICANT:

APPLICANT: Muller-Schilling, Martina

Oren, Moshe

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: Sequence 32, Application US/09834291
PATENT NO. US20020042064A1
: GENERAL INFORMATION:
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
            APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2001-08-21
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PRIOR APPLICATION NUMBER: PCT/DE99/03343
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LENGTH: 20
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PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
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ORGANISM: Homo Sapiens
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APPLICANT: Krammer, Peter
APPLICANT: Kuller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: D5 198 47 779.1
PRIOR APPLICATION NUMBER: D5 198 47 779.1
PRIOR APPLICATION NUMBER: D5 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
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Patent No. US20020042064A1
                 SOFTWARE: Patentin Ver. EQ ID NO 3
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
TENORUS. 770
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LENGTH: 2380
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Patent No. US20020042064A1
GENERAL INFORWATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Krammer, Peter APPLICANT: Muller-Schilli APPLICANT: Oren, Moshe
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PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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Sequence 4, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
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                                                                                                                            PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SCOTTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 3212
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SEQ ID NO 4
LENGTH: 2827
                                                                              US-09-834-291-1
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09834291
Patent No. US20020042064A1
Best Local Similarity Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                APPLICANT: Muller-Schilling, Martina AppLICANT: Oren, Moshe TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Krammer, Peter APPLICANT: Muller-Schill: APPLICANT: Oren, Moshe
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
                                                                                                TYPE: DNA
ORGANISM: Homo Sapiens
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      Conservative
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100.0%; Pred. No. 1.2;
      100.0%; Score 20; DB 9; Length 3212; 100.0%; Pred. No. 1.2; Length 3212; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
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                                                                                                                                                                                                         FILE REFERENCE: 4121-122
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1908-10-16
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                                                                                                                                                        US-09-834-291-7
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Patent No. US20020042064A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                             Matches
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Krammer, Peter APPLICANT: Muller-Schilling, Martina APPLICANT: Oren, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 20
                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                Local Similarity
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                                    1 GGACAAGCCCTGACAAGCCA 20
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                                                                                                84.0%; Score 16.8;
90.0%; Pred. No. 46
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Pred. No. 7.4;
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                                                                                     Mismatches
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                                                                                                                            DB 9; Length 20;
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US-09-834-291-9

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GRGANISM: Human
FRATURE:
FRATU
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                                                                                     Matçhes
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                                                                                                                          Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Patent No. US20020042064A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1999-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 2940917
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 32
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1 GGACAAGCCCTGACAAGCCA 20
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                                                                             Conservative
                                                                                                          84.0%; Score 16.8;
90.0%; Pred. No. 46;
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Pred. No. 46;
0; Mismatches
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APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 2743
LENGTH: 433
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                                                            Matches
                                                                                            Query Match
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Patent No. US20020137160A1
GENERAL INFORMATION:
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US-09-728-444-1101/c
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020161207A1el Murine Polynucleotide Sequences
FILE REFERENCE: LEX-0100-USA
CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1206
SOPTWARE: FastSEQ for Windows Version 4.0
LENCTH. ELECTION OF 1101
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                                                                                                                                   OTHER INFORMATION: Clone ID: 13-LIB3058-025-Q1-K1-D1
                                                                                                                                                                          ORGANISM: Bos taurus
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                                                                                                                                                                    FEATURE:
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APPLICANT:
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OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc feature
LOCATION: (1)...(516)
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                                                                           Local Similarity
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                                                      16;
4 CAAGCCCTGACAAGCC 19
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                                                        Conservative
                                              100.0%; +1
                                            80.0%; Score 16; DB 10; 100.0%; Pred. No. 1.2e+0; ive 0; Mismatches
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94.4%;
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Pred. No. 74;
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                                                                 1.2e+02;
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                                                                             Length 433;
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                                              Indels
                                          0; Gaps
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RESULT 15
US-09-878-574-9518
US-09-878-574-9518
US-09-878-574-9518
J. Sequence 9518, Application US/09878574
Patent No. US20020110548A1
PAPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT PLILING DATE: 2001-12-21
CURRENT PLILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR TILING DATE: 199-06-14
VUMBER OF SEG ID NOS: 15775
J. PRIOR THING DATE: 1999-06-14
VUMBER OF SEG ID NOS: 15775
J. PRIOR THING DATE: 1999-06-14
J. PRIOR APPLICATION Clone ID: 701102580H1
US-09-878-574-9518
LENGTH: 1655
PRIOR THING DATE: 1999-06-14
J. PRIOR THING DATE:
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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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10468.541 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted  $\dot{p}y$  chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1 AXO26100 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	C 44.4	C 411	0 0 0 2 2 2 3 2 2 3		 	321	C 298	c 26			c 20 21	18 19	16 17	C 15	c 13	c 11	109	8 7	თს	n 42 (	w N	4	Result No.	
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                                 Mueller-Schilling, M., Krammer, P. and Oren, M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 26 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 18 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Score 20; DB 9; Length 2344;
Local Similarity 100.0%; Pred. No. 2.6;
les 20; Conservative 0; Mismatches 0; Indels 1
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                                                                                    161 AGAGATGCCCAAACTGTTTT 180
2827 bp
Sequence 4 from Patent DE19847779
                                                                                                                 1 AGAGATGCCCAAACTGTTTT 20
                  AX026092
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="basal promoter"
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/chromosome="10"
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/mol type="genomic DNA"
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 4 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                     44 AGAGATGCCCAAACTGTTTT 63
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens (human)
Homo sapiens
                                                            Sequence 1262 from Patent WO03008583. AX695635
                                             AX695635.1 GI:29418787
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784 c 809 g 84
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requests: clonerequest@sanger.ac.uk
n Aug 31, 2001 this sequence version replaced gi:14161146.

During sequence assembly data is compared from overlapping clones.

During sequence sare found these are annotated as variations where differences are found these are annotated as variations the coverlapping clone name. Note that the together with a note of the overlapping clone name what the corresponding to the overlapping clone as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with an alternate chemistry or covered by high quality data (i.e., phred quality sequences was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality sequencing problems, such 30); an attempt was made to resolve all sequencing problems, such 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations of found at the complex primary accession numbers given the primary accession numbers given ababases can be found at the primary accession on the WORMPEP in the primary accession on the wormper of the primary accession on the wormper the primary accession on the wormp
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Human DNA sequence from clone RPI1-399019 on chromosome 10,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13226 a
This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The true right end of clone RP11-304I5 is at 18704 in this sequence. Location/Qualifiers
                                                                                                                                                                                                        RP11-399019 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                              http://www.chori.org/bacpac/home.htm
                                                                                                                                            VECTOR: pBACe3.6
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ORS
MUZNY, D. Martie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Aydeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Caller, R., Caver, M., Burch, P., Burch, P., Bursh, H., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Escotto, M., Edgene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Glerra, M., Goster, M., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Haddun, S. L., Hodgson, A., Hogues, M., Guerra, M., Guevara, M., Hernandez, R., Hines, S., Hilyk, S., Hune, J., Idlebird, D., Jackson, A., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewsh, L., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Martin, R., Martin, C., Mozre, S., Mozgan, M., Morris, K., Morris, C., Neal, D., Okwuonu, G., Olarnounsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., M., Mall, M., Malloy, C., Meal, D., Malloy, M., Malloy, C., Meal, D., Mozgan, M., Malloy, C., Mozgan, M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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193566 bp DNA linear HTG 28-MAR-2.
Rattus norvegicus clone CH230-135C19, WORKING DRAFT SEQUENCE, 64
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105973. .105989
/note="Sequence confirmed by AC015461 sequenced by WIBR."
55669 a 36398 c 36888 g 58358 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11.2"
100119. .100156
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/db_xref="taxon:9606"
/chromosome="10"
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="RP11-399019"
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VERSION

ORIGIN

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Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Scott, G., Stiter, C.D., Smajs, D., Sneed, A., Sodergren, E., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Yatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, J., Warren, J., Walker, M., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dumn, D., von Niederhausern, A., Weiss, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 64 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 28, 2003 this sequence version replaced gi:29165510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: phrap; version 0.990329 Consensus quality: 159659 bases at least Q40 Consensus quality: 169659 bases at least Q30 Consensus quality: 166864 bases at least Q20 Estimated insert size: 166404; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: KEON
Center clone name: CH230-135C19
Center clone name: Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 193566)
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Contact: hgsc-help@bcm.tmc.edu
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contig of 1891
contig of unknown
contig of 1084
gap of unknown
contig of 1589
                                                                                                                                                                                                                              gap of contig
                                                                                                                                                                                                                                                                                  contig of 1025 bp in length
gap of unknown length
contig of 1132 bp in length
gap of unknown length
contig of 1241 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                    where differences are found these are annotated as variations where differences are found these are annotated as variation the together with a note of the overlapping clone name. Note that the together with a note of the overlapping clone, as we submit sequence submission variation annotation may not be found in the sequence submission only a small overlap as described above.

Only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequencing problems, such 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the one plasmid subclone or more than one MI3 subclone; and the abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given databases can be found at the feature table with their source databases: Em:, EMBL; Sw:, in the feature table with their source databases: em: accession on the worwper database can be found at the feature table with their source databases.
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AL513364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 16, 2001 this sequence version replaced gi:16944088.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA sequence from clone RP11-480N10 on chromosome 1, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74951)
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                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
sections only once, except for a short overlap.
The true right end of clone RP11-480N10 is at 74951 in this sequence. The true left end of clone RP11-77G8 is at 42605 in this sequence. The true right end of clone RP11-541J2 is at 2000 in this
                                                                                                                 RP11-480N10 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                   RP11-480N10 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                             http://www.chori
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                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (20-FEB-2002) Genome Center, University of Washington,
Submitted (20-FEB-2002) Genome Center, University of Washington,
Seattle, WA 98195, USA
On Feb 20, 2002 this sequence version replaced gi:16945998.
                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Submitted (16-NOV-2001) Genome Center, University of Washington,

Submitted (16-NOV-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 163453)

3 (bases 1 to 163453)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.
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1 (bases 1 to 163453)

Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Homo sapiens chromosome 1 clone RP11-193H16, complete sequence.
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Center project name: chr-1
Center clone name: RP11-193H16 (sc0121)
Center clone name: RP11-193H16 (sc0121)
Sequencing vector: plasmid; L08752; 87% of reads
Sequencing vector: plasmid; 13% of reads
Chemistry: Dye-terminator ET; 68% of reads
Chemistry: Dye-terminator Big Dye; 32% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 163426 bases at least Q40
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                                                                                                                                                                                                                                   Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 163453)
                                                                                                                                                                                                                                                                            Web site: http://www.genome.washington.edu
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/note="Single clone region. Assembly consistent with restriction digest data."
a 14184 c 13984 g 21266 t
                                                                                                                                                                                                                --- Project Information
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/clone_lib="RPCI-11.2"
14860 ...14861
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
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Pred. No. 34;
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Quality coverage: 8.2x in Q20 bases; sum-of-contigs
                                      Consensus quality: 163453 bases at least Q30 Consensus quality: 163453 bases at least Q20 Insert size: 180697; sum-of-contigs
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Overlapping Sequences:
5': RP11-63I17 AL359971, 2000-bp overlap
3': RP4-722L13 (UWGC:sc0558) AL365355

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than

1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phremality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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REFERENCE
                                                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                     DEFINITION
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                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                         TITLE
                                                                                                                      AUTHORS
                                                                                          JOURNAL
                                                                                                                                                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 16552)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, Clone RP11-23123
                                                                                                                                                                            Homo
                                                                                                                                                                                                                                         AC024302
168522 bp DNA linear HTG 14-MAR-2000
Homo sapiens clone RP11-23123, WORKING DRAFT SEQUENCE, 18 unordered
                                                                                                                                                                                                                                                                                                                                                                   1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                              AC024302.2 GI:7239599
                                                                                                                                                                                                                                                                               AC024302
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                               (bases 1 to 168522)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment chain: 2"
54498 a 30059 c 29325 g 50484 t
                                                                                                                                                                                          HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                          sapiens
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147855
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89727
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fragment_chain:2"
131995. 134989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly fragment:01739 fragment_chain:\overline{1}" 89727. .\overline{131894}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment chai
75955. .89626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:01251
fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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. .36150
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mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75954: gap of 100 bp

89626: contig of 13672 bp in length

89726: gap of 100 bp

131894: contig of 42168 bp in length

131994: gap of 100 bp

134989: contig of 2995 bp in length

135089: gap of 100 bp

147854: contig of 12765 bp in length

147954: gap of 100 bp

147954: gap of 100 bp

165071: contig of 17117 bp in length
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95.0%;
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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                                Abraham, H., Allen, N.,
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 23 I 23

Sequencing vector: M13, M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 155724 bases at least 040 Consensus quality: 162423 bases at least 030 Consensus quality: 164971 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAr 14, 2000 this sequence version replaced gi:7108032. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                           24025
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Insert size: 166822; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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1108
2230
2330
4121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
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1107: gap of 100 bp
2229: contig of 1122 bp in length
2329: gap of 100 bp
4120: contig of 1791 bp in length
4220: gap of 100 bp
6193: contig of 1873 bp in length
6193: contig of 6463 bp in length
12656: contig of 6463 bp in length
contig of 5114 bp in length gap of 100 bp contig of 9410 bp in length gap of 100 bp
                                                                                               gap of contig
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                                                                                                                                contig of 4613 bp in length gap of 100 bp contig of 6492 bp in length
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of 6555 bp in length
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COMMENT

TITLE

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                                                             Local Similarity
145086 AGAAATGCCCAAACTGTTTT 145067
                           1 AGAGATGCCCAAACTGTTTT 20
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                                                     Conservative
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
30717. .35830
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                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
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140232. .168522
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91386. .106039
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106140. .123134
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31221 c 31549 g 49758 t
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91385: gap of 100 bp
106039: contig of 14654 bp in length
106139: gap of 100 bp
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123234: gap of 100 bp
140131: contig of 16897 bp in length
140231: gap of 100 bp
168522: contig of 28291 bp in length.
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95.0%;
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Pred. No. 3
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                                                                                                                         1705 others
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RESULT 14
BX323040
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Homo sapiens chromosome 1 clone RP11-455G22, *** SEQUENCING IN
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-ApR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Apr 25, 2003 this sequence version replaced gi:30026997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: ...-
Center code: SC
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Dye-terminator Big Dye; 19% of reads
Consensus quality: 181806 bases at least Q40
Consensus quality: 182063 bases at least Q20
Consensus quality: 182066 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator; 75% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 182435; sum-of-contigs
Insert size: 177453; 5.1% error; agarose-fp
Quality coverage: 24.55x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 24.85x in Q20 bases; sun coverage: 29.90x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. This record will be available and the accession number will as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 182635)
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180350. .182635
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                                                                                               /note="assembly_fragment:03792"
36041 c 34489 g 52341 t '
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                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
                                                                                                                                                                                                             /note="assembly_fragment:00629"
                                                                                                                                                                                                                                                                                                                                     mol_type="genomic DN/db_xref="taxon:9606"
                                                                                                                                                                                                                                                               clone_
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                                                                                                                                                                                                                                                                                                            chromosome="1"
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            92.0%;
95.0%;
                                                                                                                                                                                                                                                               _lib="RPCI-11.2"
            Score 18.4;
Pred. No. 37;
                                          DB 2;
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                                                                                                                   200 others
                                             Length 182635;
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121795 AGAAATGCCCAAACTGTTTT 121814
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Center clone name: RP23-15A13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.cshl.org/genseq
Contact: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (11-NOV-2000) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: CSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manmalla; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Manmalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 236685)

McCombie, W.R., Baker, J.P., Bahret, A., Bal, H., Balija, V., Bedhia, N.N., de la Bastide, M., Huang, E.N., King, L., Kirchoff, K.A., Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Toth, K., Vil, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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236685 bp DNA linear HTG 03-FEB-2001
Mus musculus clone RP23-15A13, WORKING DRAFT SEQUENCE, 35 unordered
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2323: contig of 22323 bp in length
22432: gap of unknown length
42140: contig of 19708 bp in length
42249: gap of unknown length
58002: gap of unknown length
72097: contig of 1644 bp in length
72097: contig of 14095 bp in length
72106: gap of unknown length
85432: contig of 13226 bp in length
85431: gap of unknown length
85431: gap of unknown length
98091: contig of 1226 bp in length
98091: contig of 12426 bp in length
110628: contig of 12426 bp in length
110735: gap of unknown length
110735: gap of unknown length
11981: contig of 12426 bp in length
11981: gap of unknown length
11981: gap of unknown length
128948: gap of unknown length
128948: gap of unknown length
13770: contig of 8849 bp in length
137578: gap of unknown length
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                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                            1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-15A13"
58998 a 57976 c 57568 g 58324 t
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181653: gap of unknown length
186153: gap of unknown length
186814: contig of 5161 bp in length
186222: gap of unknown length
191771: contig of 4249 bp in length
191771: contig of 4228 bp in length
191279: gap of unknown length
195507: contig of 4228 bp in length
195615: gap of unknown length
199316: gap of unknown length
100891: contig of 3375 bp in length
202799: gap of unknown length
202799: gap of unknown length
202653: gap of unknown length
206645: contig of 3346 bp in length
206653: gap of unknown length
209654: contig of 3301 bp in length
212567: contig of 3301 bp in length
212567: contig of 2905 bp in length
212567: gap of unknown length
212567: gap of unknown length
21350: contig of 2827 bp in length
21458: gap of unknown length
221458: gap of unknown length
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233333: contig of 2008 b
233441: gap of unknown 1
235387: contig of 1946 b
235495: gap of unknown 1
23685: contig of 1190 b
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226669: contig c
226777: gap of u
229025: contig c
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95.0%; Pred. No. 38
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152662: contig of 6721 bp in length
152770: gap of unknown length
158664: contig of 5894 bp in length
158772: gap of unknown length
164620: contig of 5848 bp in length
164728: gap of unknown length
170566: contig of 5838 bp in length
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REFERENCE AUTHORS

TITLE JOURNAL

JOURNAL

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AUTHORS

SOURCE KEYWORDS

ORGANISM

ACCESSION DEFINITION AC084744/c

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Matches

19; Conservative

0; Mismatches

1; Indels

COMMENT

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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2003 Compugen; Ltd.
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## ALIGNMENTS

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RESULT 1
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Danio rerio (zebrafish)
                                                                                                                                                                     Contact: Peng U
Lab of Functional Genomics
Institute of Molecular and Cell Biology
Ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Peng, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unique zebrafish EST clusters from two cDNA libraries
/organism="Danio rerio"
/mol_type="mRNA"
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                                                                                                                                                                                                                        Carninci, P., Nishiyama, Y., Westtover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Y. and Hayashizaki, Y., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, System. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                           further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hirooka, T., Hirozane, T., Hodoyama, Y., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kawai, J., Kojina, Y., Konno, Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, X., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka Yoshiki, A., Muramatsu, M. and Hayashizaki, Y. Sunishi, A., Yoshida, K., RIKEN Mouse ESTS (Aizawa, K. et al. 2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-03-9222
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                                                                                                                                                                                    Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB573416 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930501C15 5', mRNA sequence.
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                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                            /clone="4930501C15"
                                                  db_xref="taxon:10090"
                                                                                                                                                              Location/Qualifiers
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/clone_lib="PJR-Z1+Z2"
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/tissue_type="whole embryo or fish"
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/db_xref="taxon:7955"
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RESULT 3
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                                                                                                                                                                                                                                                               Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
                                                                                                                                                                                                                      Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer
                                                                                                                                                                                                                                                                                                                                                                     Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L., H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C. A Gene Expression Screen in Oryza sativa
                                                                                                                                                                                                                                                           Fax: 0086-571-86961525
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM420516 475 bp mRNA linear EST 28-JAN-200: U013C07 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone U013C07, mRNA sequence.
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M.grisea | M.grisea | /note="Vector: pSport2" | 109 g 1
                                             /clone_lib="Oryza sativa mature leaf library induced by
                                                                         /dev_stage="Mature stage"
                                                                                                                  /organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="U013C07"
                                                                                               /tissue_type="leaf"
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
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Pred. No. 3e+02;
0; Mismatches 1; Indels 0
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL963961.1 GI:25787556
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1 (bases 1 to 635)
1 raylor,R., Ashurst,J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sanger Xenopus tropicalis EST project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TROPICALIS_SEQUENCE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mani: trop@sanger.ac.uk
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
Sanger Xenopus tropicalis EST project 2001
TopofCALIS SEQUENCE_ID: TGas111h03.plkSP6
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                                                                                                                                                                                                      178 GAGATGCCCAAACTGTTCT 160
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                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                     2 GAGATGCCCAAACTGTTT 20
                                                                                         677 bp mRNA linear EST 01-APR-2001
BG410123
S10-8-A10 Stage 10+ Gastrula Library Xenopus laevis cDNA 5' similar
to Xenopus EST, mRNA sequence.
              xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                               BG410123.1 GI:13506129
                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="XGC-gastrula" coll All-blue"
/clone_lib="XGC-gastrula" | EcoRI; Site 2: NotI; cDNA
/note="Vector: pCS107; Site_1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
was oligo dT primed from 5ug of poly A+ RNA from lighted
10-13 gastrulae. EcoRI NotI cut cDNA was then lighted
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XII-blue"
//lab_host="coli XII-blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="taxon:8364"
'clone="TGas111h03"
                                                                                                                                                                                                                                                                                                                                                            110 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type="mRNA"
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                197 g
                                                                                                                                                                                                                                                                                                 Score 17.4; pB 9; Length 635; pred. No. 4.6e+02;
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1 (bases 1 to 677)

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The Rockefeller University
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Fax: 212 327 8685
Plate: $10-8 row:
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Seg primer: SP6-22 5' ctt gat tta ggt gac act ata g 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 GÁGATGCCCAÁACTGTTCT 28
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Similarity 94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB630820 RIKEN full-length enriched, 16 days neon musculus cDNA clone A130029G22 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Koya, S., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki Okazaki, Y., Okido, T., Salto, R., Sakai, T., Sogabe, Y., Sızuki, H., D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., Muramatsu, M. and Hayashizaki, Y., Muramatsu, M. and Hayashizaki, Y., et al. 2001)
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1 (bases 1 to 735)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Konno, Fukuda, S., Furuno, M., Fukuda, S., Furuno, M., Fukuda, S., 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap.
Tel: 81-45-503-9222
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                        Yokohama, Kanagawa 230-0045, Japan
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d, 16 days neonate thymus
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DEFINITION
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                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                            316 AGAGCTGCCCAAACTGTTT 298
                    AG-ND-165J5.TF ND-TAM Anopheles gambiae genomic clone AG-ND-165J5,
BH393256
BH393256.1 GI:17339397
                                                                                                                                                                                  1 AGAGATGCCCAAACTGTTT 19
                                                                                                                                                                                                                                                 10;
                                                                                BH393256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) further details. web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) K.K., Pukuda, S., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa Havashiyaki, V., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh. M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to genes. Genome Res. 10 (10), 1617-1630 (2000) wagt, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., S., Kawai, J., Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura Havashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                         /note="Site 1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A130029G22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="thymus"
/dev_stage="16 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
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1. .735
                                                                                                                                                                                                                                 87.0%; Score 17.4; DB 10; Length 735; 94.7%; Pred. No. 5e+02;
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Genoscope - Centre National de Sequencage
                                Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization unpublished
                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                 762 AGAGATGCCGAAACTGTTT 780
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                           BX422214 Homo sapiens FETAL LIVER Homo sapiens EST 1
CS0DM002YII9 5-PRIME, mRNA sequence.
                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                BX422214.1 GI:30638495
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Fax: 301 838 3543

Email: bjloftus@tigr.org

This Clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The back constructed at Texas A&M University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Trendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other_GSSs: AG-ND-165J5.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the malaria mosquito Anopheles gambiae Mol. Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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/note="Vector: pECBACI; Site_1: HindIII"
164 c 178 g 227 t
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/strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Anopheles gambiae"
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5162.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Faraday Avenue Genoscope sequence ID : C$0DM002AE10QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgi-bin/cluster.cgi?seq=CSODM002AE10QP1&cluster=5162.f. Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitrogen Corporation 1600 http://fulllength.invitrogen.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGAGATGCCCAAACTGTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1035 bp mRNA linear EST 01-JUN-200:
AL575246 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI062YB12 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                         Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Livitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO62DA06QP1.
Faraday Avenue Genoscope sequence ID: CSODIO62DA06QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             on Feb 16, 2001 this sequence version replaced gi:12936226.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1035)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and enriched into the Not I and ECORY sites of the pCMVSPORT 6 cloned into the Not I and ECORY sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="FETAL LIVER"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Homo sapiens FETAL LIVER"
/tissue type="placenta cor 25-NORMALIZED"
/tissue type="placenta cor 25-NORMALIZED"
/clone Tib="Homo saplens primed with a NotI-cligo(dT)
/note="Ist strand cDNA was primed with a NotI-cligo dT)
/note="Ist strand cDNA was primed cDNA was primer. Five prime end enriched, double-strand cDNA was primer. Five prime end enriched, double-strand cDNA was primer. Five prime end cloned into the Not I and EcoR v digested with Not I and cloned into the Not I and EcoR v sites of the pcMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI062YB12"
                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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AL551725 MRNA linear EST 31-MAY-200:
AL551725 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
Clone CSODIO62YL18 3-PRIME, mRNA sequence.
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Li.W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Livitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
Invitrogen. Contact: Forgen.com/ Invitrogen Corporation 1600
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO62DF09NP1.
Faraday Avenue Genoscope sequence ID: CSODIO62DF09NP1.
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                        AZ766513 200 bp DNA linear GSS 16-FEB-200
1M0564H07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
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                                                                                                    AZ766513.1 GI:12883665
                                                                                                                                          clone UUGC1M0564H07 F, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /LISSUE type="PLACENTA COT 25-NORMALIZED"
/Clone Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/Clone Tib="Homo sapiens Primed with a NotI-oligo (dT)
/note="Ist strand cDNA was primed, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
sites of the pCMVSPORT 6 vector. 24 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001 this sequence version replaced gi:12889952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                  85.0%; Score 17; DB 9; L
100.0%; Pred. No. 9.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17;
pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 others
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                                                                                                                                                                                                               GSS 16-FEB-2001
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KEYWORDS
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                                                                                                                                                                     DEFINITION
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                                                                                                                                                                                                                         RESULT 12
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                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                     Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                               137 AGAAATGCCCAAACTGATTT 118
 Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                               AA400303
AA400303.1 GI:2054192
                                                                                                                                                 zu64a03.rl Soares_testis_NHT Homo
                                                                                                                                                                                                                                                                                     1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                             AA400303
                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0564 row: H COlumn: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA polymucleotide kinase. Adaptor oligonucleotides were adaptored to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to electrophoresis. Vector DNA was prepared from a derivative electrophoresis. Vector DNA was prepared from a derivative with adaptors complementary to the insert adaptors and adaptored vector DNA, and transformed into adaptors and adaptored vector DNA, and transformed into and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                         63 a
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/Clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Wector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="UUGC1M0564H07"
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                                                                                                                                                                                                                                                                                                                                                       90.0%;
                                                                                                                                                                                                                                                                                                                                                                             84.0%;
                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                       Score 16.8; DB 28; Length 200;
Pred. No. 5.2e+02;
0; Mismatches 2; Indels 0.
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                                                                                                                                           sapiens cDNA clone
                                                                                                                                                                   mRNA
                                                                                                                                                     EST 16-MAY-1997
                                                                                                                                     IMAGE: 742732
                                                                                                                                                                                                                                                                                                                     ٥,
                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                       KEYWORDS
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                                                                     TITLE
                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                 ORGANISM
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                   1 (basss 1 to 302)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                           25 AGAGCTGCCCAAACTGCTTT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                             BF835617.1 GI:12186834
                                                                                                                                                                                                                                                                                                           RC4-HT0890-151100-017-e11 HT0890 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                           BF835617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq.primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 291)

Hillier, Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,

Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie

"Tan, Waterston,R. and Wilson,R."

WashU-Merck EST Project 1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
   Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="IMAGE:742732"
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mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.0%; Score 16.8; DB 9; 90.0%; Pred. No. 6.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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EST 13-JAN-2001

0; Gaps

0;

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                          MEDIINE
                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                      PUBMED
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-HT0890-
151100-017-e11kt3=2000-11-15&t4=1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 17 High quality sequence stop: 302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 314)

1 (contarral, Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Costa, F.F., Magai, M.A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and S.J. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CM2-GN0165-021100-487-a03 GN0165 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags
Proc: Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                          Fax: +55-11-2707001
                                                                                                                  Tel: +55-11-2704922
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_stage="Adult"
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Pred. No. 6.4e+02;
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FEATURES
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AZ719811
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021100-487-a03&t3=2000-11-02&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 322)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ719811.1 GI:12460860
                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 161 row: H column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
                                                                                                                                                                                   Class: BAC ends.
                                                                                                                                                                                                           Seq primer: T7
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74 g 94 t
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/clone_lib="GN0165"
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/db_xref="taxon:9606"
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                      /organism="Mus muscullus"
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/mol type="578L/5J"
/strain="c578L/5J"
/db xref="taxon:10090"
/clone="RPCI-24-161H14"
/sex="Male"
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Pred. No. 6.5e+02;
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Search completed: August 1, 2003, 20:43:03
Job time: 73.4754 secs
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                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0%; Score 16.8; DB 28; Length 322;
Best Local Similarity 90.0%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps
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91 AGAAATGCCCAAAGTGTTTT 110
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/clone_lib="RPCI-24"
/notce="Wector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/notce="Wector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Pred. No score 9 and is
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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DR XX PT	X II	PAXX	P X	pę XX	X G	PN	20 2	\$ \$ \$ \$	D X	ВX	A X	RESULT AAZ887 ID A		C 44 C 45	0	C 41	10	c 37	C 36	1 134 154	33	υus	29 30	c 28			c 22	20 21	19	17		c 13	11 12	10	
WPI, 2000-162245/15. Novel receptor DNA useful for identifying a substances potentially useful for cancer ch	Krammer P, Mueller-Schilling M, Oren M;	(DEKR-)	16-OCT-1998; 98DE-1047779.	16-OCT-1998; 98DE-1047779.	03-FEB-2000.	DE19847779-C1.	Homo sapiens.	p53; CD95 receptor; human; screening; apoptor cancer chemotherapy; 88.	BILITIE		AAZ88701;	Л 1  701 AAZ88701 standard; DNA; 20 BP.	ALIGNMENTS	15.8 79.0 1195 24 ABL95531 15.8 79.0 1195 25 ACA59968	15.8 79.0 1195	15.8 79.0 1195 2	15.8 79.0 1193 2	15.8 79.0 1157 2	15.8 79.0 1157 2	15.8 79.0 714 2 15.8 79.0 714 2	15.8 79.0 458 2	15.8 79.0 451 2: 15.8 79.0 454 2:	15.8 79.0 451 23	15.8 79.0 440 23	15.8 79.0 440 23	15.8 79.0 416 23 15.8 79.0 440 23	15.8 79.0 364 23 15.8 79.0 364 23	16.4 82.0 2656 25 16.4 82.0 2656 25	16.8 84.0 349980 22 16.8 84.0 349980 22	16.8 84.0 20072 24 16.8 84.0 43795 21	16.8 84.0 20072 20 16.8 84.0 20072 20	16.8 84.0 9821 22	.8 84.0 2000 13 .8 84.0 2185 24	5.8 84.0 1569 24 2008 19	5.8 84.0 661 16
apoptosis-modulating									ais-modula	fracment #1.				ate cancer t	Human P789P CDNA 8	ע	Human prostate CDN			ec Sec	prostate	prostate	prostate	prostate prostate	Human prostate exp	Human prostate exp	Human prostate exp		Human EST-derived Brassica napus con	Human DAZ genomic	Enterococcus faeca	Human reproductive	Chromosome 13q31-q	RADS	· @ S.

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The invention relates to a nucleic acid array, where each coordinate CC contains a single nucleic acid species having one of 770 nucleotide CC sequences (appearing as ABS76747-ABS77518) a of a Xenopus embryonic gene CC product, or its complement or hybridisable fragment of not less than CC 20 contiguous nucleotides of one of those sequences. Also included are CC detecting differential expression of embryonic genes, comprising: CC contacting a nucleic acid array comprising genes expressed in CC control cells, and (b) detecting differential hybridisation of nucleic acid sfrom the sample cells with nucleic acids from sample and CC defects in development, comprising: (a) contacting nucleic acids from the sample cells relative to the control cells; and detecting products known to play a fundamental role in the development process; and CC cells relative to a standard. The invention is useful to identify genes involved in embryonic development and related process; and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes involved in embryonic development and related processes such as
                                                                                                                                                                                                                                                                                                                 Nucleic acid array containing Xenopus embryonic nucleic acids is useful to identify genes involved in embryonic development, to identify different types of embryonic cells, and to diagnose developmental
                                                                                                                                                                                                                                                                                 Claim 1; Page 763; 823pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-626534/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hemmati-Brivanlou A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2000; 2000US-219658P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JUL-2001; 2001US-0910943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2002081610-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray; cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frog; ss; embryonic_development; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frog embryonic gene sequence Q9925901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABS77493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS77493 standard; cDNA; 732 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor promoter which is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 5; 12pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGAGATGCCCAAACTGTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Altmann CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DB 21
100.0%; Pred. No. 0.89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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8
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                                                                                         Query Match
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                                                                                                                 The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY34584-Y35879. C. pneumoniae causes to be a contributing factor in heart disease, sarcoidosis, sinusitis, encoded by the open reading frames of the C. pneumoniae genome (see Vectors Can be used in immunogenic compositions as vaccines. AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
1034868 GAGATGCCAAAACTGTTTT 1034850
                                                                                           Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                  Claim 1; Page 291-611; 1912pp; English.
                                                                                                                                                                                                                                                                                                              Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-357842/30.
                                                                                                                                                                                                                                                                                                                                                                               Griffais R;
                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09927105-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of the complete genome of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX91990 standard; DNA; 1230025 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX91990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell differentiation. This would be useful for diagnosing developmental disorders and for identifying different types of embryonic cells. The present sequence is one of the 770 Xenopus embryonic cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 732 BP; 208 A; 154 C; 200 G; 169 T; 1 other;
                                                             18;
                         2 GAGATGCCCAAACTGTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 GAGATGCCCAAACTGTTCT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GAGATGCCCAAACTGTTT 20
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0107078.
97FR-0014673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-IB01890
                                                     87.0%; Score 17.4; DB 20; Length 1230025; 94.7%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.0%; Score 17.4;
94.7%; Pred. No. 37
                                                  Mismatches
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                                            Indels
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Sun Aug

AAS51323 standard; DNA; 234 BP

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AAS51323/c

IID AAS513

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AC AAS513

XX

AC AAS513

XX

Enterc

XX

Antibe

XX

Z1-MA

XX

Z1-MA

PR 23-MO

PR 23-MO
                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC genes themselves and the encoded proteins. The prokaryotes used are CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets of identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC and rooteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC a wide variety of organisms. The present sequence encodes an CC a wide variety of organisms. The present sequence encodes an CC essential prokaryotic cellular proliferation protein. CC of the printed specification, but was obtained in electronic CC format directly from MIPO at
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                                                                                                                    Matches
                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2000; 2000US-206848P-
26-MAY-2000; 2000US-207727P-
26-MAY-2000; 2000US-242578P-
27-NOV-2000; 2000US-253625P-
27-NOV-2000; 2000US-257931P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2001; 2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; Seq ID No 3905; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAU33464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                            Sequence 234 BP; 84 A; 33 C; 46 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                             ьосаі
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-611495/70.
   87 AGAAATGCACAAACTGTTT 68
                                                        1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprise sequences of antisense nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen KL,
Xu HH;
                                                                                                                          Conservative
                                                                                                                                                       90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW, Wall D, Trawick JD,
                                                                                                                              0
                                                                                                                                                          Score 16.8;
Pred. No. 63
                                                                                                                                 Mismatches
                                                                                                                                                                       63;
                                                                                                                                                                                                DB 23; Length 234;
                                                                                                                                       2;
                                                                                                                                             Indels
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                                                                                                                                                       Gaps
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RESULT 5

RESULT 6

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AAS53070/c
ID AAS530
                                                                                                                    The invention relates to antisense inhibitors of genes essential to comprove the cellular proliferation, their use in identifying the cellular proliferation, their use in identifying the censes, their use in the discovery of novel antibiotics, the essential comproverses themselves and the encoded proteins. The prokaryotes used are censes themselves and the encoded proteins. The prokaryotes used are computationally president to proteins and Enterococcus faecalis. The computation is also useful for the identification of potential new targets computed to identify proteins used in proliferation, to express these proteins. Computed to obtain antibodies capable of binding to the expressed proteins. The programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery compounds. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery model to model to acid sequence in the control of the protein collular proliferation protein.

Compound the process of the protein protein collular proliferation protein.

Compound the protein collular proliferation protein.

Compound the protein collular proliferation protein.

Compound the protein collular proliferation protein.
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                                                            Matches
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; ds; prokaryotic cellular proliferation gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis DNA for cellular proliferation protein #498.
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23-MAY-2000; 2000US-206848P:
26-MAY-2000; 2000US-207727P:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Seq ID No 6707; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                      Sequence 306 BP; 117 A; 40 C; 65 G; 84 T; 0 other;
                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-611495/70.
                                                                          ocal Similarity
105 AGAAATGCACAAACTGTTTT 86
                                                            18;
                              1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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2001US-269308P.
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Xu HH;
                                                                                  84.0%;
90.0%;
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                                                                0; Mismatches
                                                                                Score 16.8; DB 23; Length 306; Pred. No. 65;
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                                                                          2
                                                                           Indels
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                                                                                                                                                                                                                                                                                                                             The present sequence is one of a large number of 5' ESTs derived from CC identified within the present sequence. The 5' ESTs were prepared from CC total human RNAs or polyA+ RNAs derived from 3' untranslated region (UTR) CC expences usually correspond mainly to the 3' untranslated region (UTR) CC libraries. Such ESTs are not well suited for isolating cDNA sequences not well suited for isolating cDNA sequences for ends of mRNAs and even in those cases where longer CC isonated from mRNAs with intact 5' ends and can therefore be comed to obtain full length cDNAs with intact 5' ends and can therefore be comed to obtain upstream regulatory sequences and to design correspond to obtain upstream regulatory sequences and to design to expression and secretion vectors.
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                            Query Match
 'Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress;
physiclogical provocation;
                                         Bacillus licheniformis genomic sequence tag (GST) #1452.
                                                                              13-AUG-2002 (first entry)
                                                                                                                ABK74161;
                                                                                                                                 ABK74161 standard; DNA; 368 BP
                                                                                                                                                                                                                                                                                                        Sequence 338 BP; 86 A; 60 C; 42 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 22200; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J, Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein 5' EST, SEQ ID NO: 22200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC18125 standard; cDNA; 338 BP.
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                                                                                                                                                                                                              19
                                                                                                                                                                                                                              1 AGAGATGCCCAAACTGTTT 20
                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                   AGAAATGGCCAAACTGTTTT 38
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0122487
                                                                                                                                                                                                                                                                        84.0%;
90.0%;
environmental stress; ds.
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                                                                                                                                                                                                                                                                        Score 16.8;
Pred. No. 67
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Giordano J;
                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                           DB 21; Length 338;
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                                                                                                                                                                                                                                                                                                                                                                                                                          CC The invention describes a method of monitoring differential expression of CC genes in a first Bacillus cell relative to expression of the genes in CC other Bacillus cells, comprising hybridising labelled nucleic acid probes in CC isolated from Bacillus cells to a substrate containing array of Bacillus cells to a substrate containing array of Bacillus cells to a substrate containing array of Bacillus cells relative gene expression by an observed hybridisation reporter signal of common common second Bacillus cell relative to expression of the same genes in a first Bacillus cell relative to expression of the same genes common of several genes from a Bacillus cell, discovering the compression of genes, identifying possible functions of unknown open reading frames and cell myression of genes may be used to provide a representation of the way cell in expression of genes may be used to provide a representation of the way cell solution on commental stress or other physiological provocation. Extensive cequals one gene or one open reading frame, since sequence information is changes in culture conditions.

CC available. This sequence represents a genomic sequence tag (GST) used in content of the invention. but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                         Query Match
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Human; secreted protein; gene therapy; cancer; immune disease;
haemostatic disorder; hyperproliferative disorder; renal disorder;
                                                       Human secreted protein coding sequence SEQ ID NO: 59.
                                                                                               08-JUL-2002 (first entry)
                                                                                                                                        AAL45854;
                                                                                                                                                              AAL45854 standard; cDNA; 409 BP
                                                                                                                                                                                                                                                                                                                                                                           Sequence 368 BP; 133 A; 75 C; 83 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID NO 1452; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berka R,
                                                                                                                                                                                                                                                                                                                                          Local
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27-MAR-2001; 2001US-279526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVO ) NOVOZYMES BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2001; 2001WO-US31437.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200229113-A2.
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                                                                                                                                                                                                                                                 342 ÁGÁGÁTGCTCÁÁÁCTGGTTT 361
                                                                                                                                                                                                                                                                  1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                h 84.0%;
Similarity 90.0%;
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                                                                                                                                                                                                                                                                                                                                            Score 16.8;
                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                67;
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RESULT 9
AATO35
XX
AC AATO35
XX
DT 12-UUN
XX
P-Vir
KW Capsid
KW Capsid
KW Skin c
XX
KW Papill
XX
KW Capsid
KW Skin c
XX
FT Mat_be
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PF 09-NO
XX
PF 09-NO
XX
PF 04-MAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; reproductive system disorder; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200228877-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disorder; respiratory disorder; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-2000; 2000US-236326P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2001; 2001WO-US01432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of human secreted proteins. These can be used in the treatment cancer, immune diseases, haemostatic disorders, hyperproliferative disorders, renal disorders, cardiovascular disorders, respiratory disorders, neurological diseases, infections and reproductive system disorders. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-340092/37.
P-PSDB; AAO17218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 409 BP; 106 A; 62 C; 74 G; 163 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 478; 538pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                  HP-Virus 49; papilloma virus; major; capsid protein; plasmid VS40-7; DSM 9135; diagnosis; skin carcinomas; therapy; vaccination; ds.
                                                                                                                                                                                                                                                   12-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                       AAT03501 standard; DNA;
                                                                                                                                        Papilloma virus.
                                                                                                                                                                                                                      Papilloma virus major capsid protein DNA.
                               09-NOV-1995.
                                                         DE4415743-A1
                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                           AGAAATGGCCAAACTGTTTT 247
                                                                                                                                                                                                                                                                                                                                                                                                      AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fungicide; ophthalmalogical; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wei P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
     94DE-4415743.
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%;
                                                                                                                                                                                                                                                                                                          661
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Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO.
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Shi Y, Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                  69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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oi GH, Fiscella
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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ARAL45853
ID AAL45
AC AAL45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   de Villiers zur Hausen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding peptide(s) of papilloma virus major capsid protein useful for detecting papilloma virus in skin carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemostatic disorder; hyperproliferative disorder; renal disorder; cardiovascular disorder; respiratory disorder; neurological disease; infection; reproductive system disorder; immunosuppressive; antirhritic; antirhoumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 661 BP; 195 A; 118 C; 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein coding sequence SEQ ID NO: 58
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                                                                                                  WPI; 2002-340092/37.
P-PSDB; AAO17217.
                                                                                                                                                                                                                                                                                                                                         29-SEP-2000; 2000US-236326P
                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; gene therapy; cancer; immune disease;
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Wei P, Ebner R
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                Birse CE, Soppet
Shi Y, Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           661;
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for
                                                                                                                                                                                                                      DR, Olse
Fiscella
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Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition

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The present sequence represents a specifically claimed partial nucleic cacid sequence encoding human RAD54 (hRAD54). A method for analysing a consequence of at least 15 and no more than 30 consecutive bases of the DNA sequence of at least 15 and no more than 30 consecutive bases of the DNA sequence encoding hRAD54. hRAD54 is a gene thought to be present in tumours that display allelic imbalance at 1932, the chromosomal band consecutive bases of for intumours that display allelic imbalance at 1932, the chromosomal band consecutive bases of four minimal regions of chromosome 1 deletion in CC breast carcinomas. hRAD54 is useful for production of proteins, inter CC alia, that have been identified as novel hRAD54 by homology between the CC amino acid sequence given in AAW62186 and known amino acid sequences concer, including Koroderma Pigmentosum and Bloom syndrome, Werner's Syndromes and X-linked mental retardation with alpha-thalassaemia CC dyndromes and breast cancer. hRAD54 polynucleotides are also useful for CC detecting complementary nucleotides for use as a diagnostic agent, case of the complementary nucleotides for use as a diagnostic agent, case of the complementary nucleotides for use as a diagnostic agent, case of the complementary nucleotides of disease or susceptibility to diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                  Human hRAD54 DNA and polypeptide - and agonists, antibodies,
                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 27-28; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-274189/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Croce CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYJE-) UNIV JEFFERSON THOMAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; RAD54; hRAD54; cancer; xeroderma pigmentosum; Bloom syndrome; werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily; X-linked mental retardation with alpha-thalassemia syndrome; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human secreted proteins. These can be used in the treatment cancer, immune diseases, haemostatic disorders, hyperproliferative disorders, renal disorders, cardiovascular disorders, respiratory disorders, neurological diseases, infections and reproductive system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV39297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 478; 538pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 AGAAATGGCCAAACTGTTTT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAD54 nucleic acid sequence comprising exons 5-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robbins DJ;
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RESULT 12
AAL45822
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                               Matches
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                                                                                                                      The present invention provides the protein and coding sequences of a number of human secreted proteins. These can be used in the treatment cancer, immune diseases, haemostatic disorders, hyperproliferative disorders, renal disorders, cardiovascular disorders, respiratory disorders, neurological diseases, infections and reproductive system
                                                                                Sequence 2185 BP; 613 A; 302 C; 320 G; 950 T; 0 other;
                                                                                                           disorders. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                Claim 1; Page 458-459; 538pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; gene therapy; cancer; immune disease; haemostatic disorder; hyperproliferative disorder; renal disorder; cardiovascular disorder; respiratory disorder; neurological disease; infection; reproductive system disorder; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacteri;
                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-2000; 2000US-236326P
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-2001; 2001WO-US01432
                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL45822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins are useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hRAD54 polynucleotide, proteins, agonists and antagonists which
                                                                                                                                                                                                                                                                                                       2002-340092/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 AGAGATGCCCAAACTGAGTT 158
1 AGAGATGCCCAAACTGTTTT 20
                               18;
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                                             Similarity
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                              Conservative
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                                        84.0%;
90.0%;
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Duan DR,
                                                      Score 16.8;
                                          Pred.
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Pred. No. 9
                           Mismatches
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Shi Y, Choi
                                                   DB 24; Length 2185;
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hoi GH, Fiscella M;
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AGAAATGGCCAAACTGTTTT 247

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RESULT 13
AAHS17
XX AAHS17
XX 29-AUG
XX 29-AUG
XX 8bg1;
XX bialli
XX Nocool
XX 8bg1;
XX Nocool
XX 8bg1;
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XX Nocool
XX 10-AB
PR 30-AB
PR 30-AB
PR 29-JU
PR 
                                                                                                                                           AAH51601 represents a human genomic nucleotide sequence comprising sbg1, cc g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the CC biallelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and CC biallelic markers and polymorphisms. Sequences AAH51602 - AAH51627 - AAH51
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biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides comprising sequences from sbg1 and g35018 biallelic markers are used for genotyping and detecting schizophrenia or bipolar disorder and predisposition to these disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 643-644; 737pp; English.
                                                                                           Sequence 3001 BP; 842 A; 608 C; 584 G; 966 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0126903.
99US-0131971.
99US-0132065.
99US-0143928.
99US-0145915.
99US-0146452.
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99US-0162288.
          84.0%;
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              Score 16.8; Pred. No. 96;
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                                                      ps 21; Length 3001;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human reproductive system related antigen DNA SEQ ID NO: 5933.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; gene therapy; ds.
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24-FEB-2000;
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                                    01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
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14-AUG-2000;
              05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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14-AUG-2000;
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23-AUG-2000;
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2000US-0229513.
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08-SEP-2000; 2000US-0231243. 08-SEP-2000; 2000US-0231244. 08-SEP-2000; 2000US-0231413. 08-SEP-2000; 2000US-0231414. 08-SEP-2000; 2000US-0232080.

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XX WO2001:
XX WA FEB
PR 02-MAR
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-018464.
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                                                                                                                  02-AUG-2001.
                                                                                                                                          WO200155320-A2
                                                                                                                                                                                          Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                        Human reproductive system related antigen DNA SEQ ID NO: 5934.
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01-DEC-2000; 2000US-0250160;
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05-DEC-2000; 2000US-0251988;
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08-DEC-2000; 2000US-0251869;
08-DEC-2000; 2000US-025199;
                                                                                                                                                                                                                                                               21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                               AAL03246;
                                                                                                                                                                                                                                                                                                                 AAL03246 standard; DNA; 9824 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9821 BP; 3056 A; 1735 C; 1689 G; 3341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 5933; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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20-OCT-2000; 2
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                                                                                                                                Disclosure; SEQ ID NO 5934; 1297pp + Sequence Listing; English.
                                                                                                                                                                                 Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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   August 1, 2003, 08:05:17 ; Search time 5.18607 Seconds (without alignments)
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                                        Sequence 5934, Ap
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                       Sequence
Sequence
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APPLICANT: OTEN, MOSHE
TITLE OF INVENTION: P53 Binding Areas
TITLE OF INVENTION: P53 Binding Areas
TITLE APPLICATION NUMBER: US/99/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 199-10-18
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16 Patent No. US20020042064Al
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
APPLICANT: Oren, Moshe RESULT 1 US-09-834-291-12 sequence 12, Application US/09834291 patent No. US20020042064A1 ORGANISM: Homo Sapiens US-09-834-291-12 밁 RESULT 2 SEQ ID NO 12 LENGTH: 20 Query Match Best Local Similarity Matches 20; Conserv Conservative 100.0%; Score 20; DB 5 0 Mismatches DB 9; Length 20;

0

Gaps

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Sequence 18, Application U sequence 18, Application U US20020042064A1; GENERAL INFORMATION:

APPLICANT: Krammer, Peter

US-09-834-291-18

Application US/09834291

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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
FILE Oren, Moshe
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
                                                                                                                                               US-09-834-291-4

Sequence 4, Application US/09834291

Patent NO. US20020042064A1

GENERAL INFORMATION:

Peter
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US-09-834-291-26
Sequence 26, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION; Peter
Krammer, Peter
Martin
                                                                                                                                                                                                                                                                                RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
TITLE OF INVENTION: p53 Binding Areas
CURRENT APPLICANTE: MULLER 2001-08-21
CURRENT APPLICATION NUMBER: US/09/834,291
FRIOR APPLICATION NUMBER: PCT/DE99/03343
FRIOR APPLICATION NUMBER: PCT/DE99/03343
FRIOR APPLICATION NUMBER: DE 198 47 779.1
FRIOR FILING DATE: 1999-10-18
FRIOR FILING DATE: 1999-10-16
SOFTWARE: PATENT DATE: 1999-10-16
FRIOR FILING DATE: 1999-10-16
FRIOR SEQ ID NOS: 32
FRIOR SEG ID NOS: 32
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US-09-834-291-26
PRIOR_APPLICATION NUMBER: PCT/DE99/03343
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i PRIOR APPLICATION NUMBER: 2001-08-21
i PRIOR APPLICATION NUMBER: PCT/DE99/03343
i PRIOR FILING DATE: 1999-10-18
i PRIOR FILING DATE: 1999-10-18
i PRIOR FILING DATE: 1998-10-16
i NUMBER OF SEQ ID NOOS: 32
i SEQ ID NO 18
i PRIOR NO 18
i PRIOR SECTION PORTON SECULORISTICATION NUMBER: DE 198 47 779.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapiens US-09-834-291-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 40;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Muller-Schilling, Martina APPLICANT: Oren, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 4121-122
                                                                                                                                                                                                                                                                                                               1 AGAGATGCCCAAACTGTTTT 20
|||||||||||||||||
11 AGAGATGCCCAAACTGTTTT 30
                                                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 9;
100.0%; Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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CURRENT APPLICATION NUMBER: US/09/910,943
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 742
SOFTWARE: PatentIn version 3.1
LENGTH: 732
                                                                                                                                                                                                                Sequence 719, Application US/09910943 Fatent No. US20020081610A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   US-09-910-943-719/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
TITLE OF INVENTION. p53 Binding Areas
CURREWT APPLICATION NUMBER: US/09/834,291
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: D5198 47 779.1
NUMBER OF SEQ ID NOS.
SOFTWARR: DATE: 1998-10-16
NUMBER OF SEQ ID NOS.
SOFTWARR: DATE-HING DATE: 1998-10-16
                                                                                                                             APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Altman, Curris
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/1G148US1
                                 TYPE: DNA
ORGANISM: Xenopus laevis
NAME/KEY: misc feature LOCATION: (1)...(732)
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09834291
Patent No. US20020042064A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 4
LENGTH: 2827
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100.0%; Pred. No. 1.:
% Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 3212;
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US-09-834-291-13
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-13
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRICATION NUMBER: 60/206,848
PRIOR PRICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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Patent No. US20020061569A1
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TITLE OF INVENTION: 953 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n may be a or g or c or t/u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                               APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith V
                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITEA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 87.0%;
Local Similarity 94.7%;
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Local Similarity 90.0%;
les 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09834291
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No. 2
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Pred. No. 25
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US-09-815-242-3905
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/11,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-7
PRIOR PILING DATE: 2000-12-7
PRIOR PILING DATE: 2000-12-7
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; sequence 6707, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 3905
                                                                                                                                                         ; LOCATION: (1).
US-09-815-242-6707
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APPLICANT: Ohlsen, K
APPLICANT: Zyskind,
                                                                                                                                                                                                                                                                                                      SEQ ID NO 6707
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                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecalis
                                                                                                  Best
                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                   ENGTH:
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  105 AGAAATGCACAAACTGTTTT 86
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                                          1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                   306
                                                                                 18;
                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr, Grant
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                                                                                   Conservative
                                                                                                                                                                               ... (306)
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                                                                                                    84.0%; Score 16.8;
90.0%; Pred. No. 42;
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                                                                                     0,
                                                                                     Mismatches
                                                                                                                             DB 9; Length 306;
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                                                                                                                                                                                                                                                                                                                      US-10-027-632-205156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 205156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 205156, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-974-300-1452
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE OF INVENTION: EXPRESSION CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gr
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
70 AGAAATGTCCAAACTGTTTT 89
                                                         1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 AGAGATGCTCAAACTGGTTT 361
                                                                                                                                                         18; Conservative
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                                                                                                                                                                                  84.0%; Score 16.8;
90.0%; Pred. No. 49
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Pred. No. 4
                                                                                                                                                Mismatches
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Sequence 5933, Application US/09764891

Publication No. US20030077808A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 5933
LENGTH: 9821
Type: Num
                                                                                                                                                                                                                                                            US-09-070-927A-89
                                                                                                                                                                                                                                                                                  RESULT 14
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; Sequence 5934, Application US/09764891
; Publication No. US20030077808A1
                                                                                                                                                                                                     Sequence 89, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
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LENGTH: 9824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                 TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                             APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                      2800 AGAGCTGCCCAAACTGCTTT 2781
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STATE: Maryland COUNTRY: USA
                                   CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 8
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GENERAL INFORMATION:

APPLICANT: HYSEG, Inc.

FITTLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: PASTSEQ for Windows Version 3.0

SEQ ID NO 1867

LENGTH: 472

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-918-995-1867
; Sequence 1867, Application US/09918995
; Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-09-070-927A-89
                        Ş
                                                                                                                                            ; FEATURE:

, NAME/KEY: misc_feature

; LOCATION: (1)...(472)

; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-1867
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SEQUENCE CHARACTERISTICS:
LENGTH: 20072 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                       Query Match
Best Local (
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                                                                    Matches
                                                               y Match 79.0%; Score 15.8; DB 11; Local Similarity 89.5%; Pred. No. 1.6e+02; hes 17; Conservative 0; Mismatches 2;
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FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
COMPUTER: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7383 AGAAATGCACAAACTGTTTT 7402
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2 GAGATGCCCAAACTGTTTT 20
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Pred. No. 96;
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Db 73 GAGATGCCCTACCTGTTTT 91

Search completed: August 1, 2003, 13:36:57 Job time : 6.18607 secs

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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2 6/ptodata/1/ina/5B_COMB.seq:*
/cgn2 6/ptodata/1/ina/6A_COMB.seq:*
/cgn2 6/ptodata/1/ina/6B_COMB.seq:*
/cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2 6/ptodata/1/ina/backfiles1.seq:*
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US-09-134-001C-2038 | US-09-134-001C-2 | US-08-578-634C-2 | US-09-430-010-2 | US-09-221-0178-753 | US-09-221-0178-753 | US-09-221-0178-753 | US-09-499-203-14 | US-09-499-203-17 | US-09-499-203-17 | US-09-499-203-1
                                                                                                                  US-09-198-452A-1
US-08-578-634C-3
US-09-430-010-3
US-09-430-010-3
US-09-539-333D-162
US-08-742-185-101
US-09-323-873A-6
US-09-323-873A-6
US-09-311-752-13
US-09-311-752-13
US-09-311-752-13
US-08-487-183A-13
US-08-487-183A-13
US-08-460-934-8
US-08-460-934-8
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US-08-916-4218-1
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5347.959 Million cell updates/sec
                                                                                                   sequence 1, Appli
Sequence 1, Appli
Sequence 2038, Ap
                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                         Sequence 15, Appl
Sequence 13, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 8, Appli
Sequence 8, Appli
                                     Sequence 2, Appli
Sequence 2, Appli
Sequence 753, App
Sequence 1283, App
Sequence 14, Appl
Sequence 20, Appl
                                                                                                                                                                                                                                                                                  Sequence 3, Sequence 3,
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Sequence 162, App
Sequence 101, App
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              Sequence
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      Sequence
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                                                                                                                                                                                          1, Appli
6, Appli
7, Appli
13, Appl
15, Appl
13, Appl
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28 15.2 76.0 148567 4 US-09-801-876B-3 30 15.2 76.0 319608 4 US-09-839-333D-1 31 15.2 76.0 319608 4 US-09-839-333D-1 32 14.8 74.0 432 4 US-09-641-638-435 33 14.8 74.0 495 3 US-09-109-204-20 41 14.8 74.0 605 3 US-09-109-204-19 36 14.8 74.0 605 3 US-09-109-204-19 36 14.8 74.0 605 4 US-09-490-032-20 37 14.8 74.0 1001 4 US-08-941-317-240 38 14.8 74.0 1001 4 US-08-941-317-240 39 14.8 74.0 2125 3 US-09-109-204-5 40 14.8 74.0 3794 4 US-09-68821-1 41 14.8 74.0 3794 4 US-09-68821-1 42 14.8 74.0 3804 4 US-09-688-831-1 43 14.8 74.0 26664 4 US-09-521-0178-577 44 14.8 74.0 26664 4 US-09-521-0178-577 44 14.8 74.0 26664 4 US-09-521-0178-577 44 14.4 72.0 8832 1 US-08-473-496-1
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US-09-801-876B-3 US-09-813-33D-1 US-09-673-409-1 US-09-671-638-435 US-09-109-204-20 US-09-109-204-19 US-09-490-032-20 US-09-490-032-19 US-09-671-317-240 US-09-671-317-240 US-09-671-317-240 US-09-671-317-240 US-09-68B-81-1 US-09-68B-81-1 US-09-68B-81-7 US-09-68B-81-7 US-09-68B-81-7 US-09-564-805-28 US-09-564-805-28 US-09-564-805-28

## ALIGNMENTS

RESULT 1 US-09-198-452A-1/c

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Sequence 1, Application US/09198452A Patent No. 6559294 GENERAL INFORMATION:
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                                                                                                                                                                                        NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (45001)..(60000)
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LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (75001)..(90000)
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NAME/KEY: misc_feature
LOCATION: (90001)..(105000)
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
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CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6849
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LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or
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NAME/KEY: misc_feature
LOCATION: (1)...(15000)

OTHER INFORMATION: n=a or c
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                                                                   NAME/KEY: misc feature
LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
LOCATION: (135001)..(150000)
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OTHER INFORMATION: n=a or c or NAME/KEY: misc_feature LOCATION: (150001)...(165000)
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LOCATION: (37501)..(390000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (390001)..(405000)
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NAME/KEY: misc feature
LOCATION: (39001)..(405000)
OTHER INFORMATION: n=a or c or g or t
LOCATION: (405001)..(420000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (450001)..(465000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (465001)..(480000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (495001)..(510000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (480001)..(495000) OTHER INFORMATION: nea or c or g or t NAME/KEY: misc\_feature LOCATION: (420001)...(435000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc\_feature LOCATION: (435001)...(450000) OTHER INFORMATION: n=a or c or g or t JOCATION: (510001)..(525000)

THER INFORMATION: n=a or c or g or t LOCATION: (345001)...(360000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (360001)...(375000)
OTHER INFORMATION: n=a or c or g or t OTHER INFORMATION: n=a or c or g or OCATION: (315001)..(330000)
OTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature LOCATION: (285001)..(300000) OTHER INFORMATION: n=a or c or g AME/KEY: misc feature NAME/KEY: misc\_feature LOCATION: (255001)..(270000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc\_feature LOCATION: (225001)..(240000) OTHER INFORMATION: n=a or c or g or t OCATION: (300001)..(315000)
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OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc\_feature
LOCATION: (735001)...(750000)
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LOCATION: (750001)...(765000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc\_feature
LOCATION: (765001)...(780000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc\_feature NAME/KEY: misc\_feature
LOCATION: (67501)...(69000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc\_feature
LOCATION: (69001)...(705000)
OTHER INFORMATION: n=a or c or g.or t
NAME/KEY: misc\_feature
LOCATION: (70501)...(720000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc\_feature
LOCATION: (70501)...(720000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc\_feature
LOCATION: (720001)...(735000) LOCATION: (63001)..(64500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (645001)..(660000)
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NAME/KEY: misc feature
LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (66001)..(675000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (675001)..(690000) NAME/KEY: misc feature LOCATION: (870001)..(885000) OTHER INFORMATION: n=a or c or g or t DTHEM AND GENERAL PROPERTY OF THE PROPERTY OF NAME/KEY: misc\_feature LOCATION: (855001)...(870000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature
LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc\_feature NAME/KEY: misc feature LOCATION: (780001)...(795000) OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature LOCATION: (795001)...(810000) OTHER INFORMATION: n=a or c or g or t LOCATION: (825001)..(840000)
OTHER INFORMATION: n=a or c LOCATION: (58501)...(600000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (600001)...(615000)
OTHER INFORMATION: n=a or c or g or t LOCATION: (615001)...(630000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc\_feature NAME/KEY: misc feature LOCATION: (570001)..(585000) OTHER INFORMATION: n=a or c or g or t LOCATION: (540001)..(555000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (555001)..(570000)
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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
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                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: 26-JAN-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                            Matches
                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA TITLE OF INVENTION: VIRUS MAIN CAPSIDE PROTEIN AND USE THEREOF
                                                                                                                                                                                                                     TELEFAX: (650)493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 493-4935
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            FEATURE:
                                                                                                                                        MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                         NAME: Abrams, Samuel B. REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 841
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                NAME/KEY:
                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                            LENGTH: 661 base pairs
                                        Local Similarity
                                                                                                   LOCATION:
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                                                                                                                                                                                                                                                     (650) 493-5556
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                                  84.0%; Score 16.8; DB.3; Length 66 90.0%; Pred. No. 9.2; 1ndels 1tive 0; Mismatches 2; Indels
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pred. No. 1
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                                                                  DB:3; Length 661;
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                                     Sequence 162, Application US/09539333D Patent No. 6476208 GENERAL INFORMATION:
                                                                                    RESULT 4
US-09-539-333D-162/C
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APPLICANT: Ethel Michele De V
APPLICANT: Zur Hausen
APPLICANT: Irene Leigh
APPLICANT: Harald Zur Hausen
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA CODING FOR A PEPTIDE OF A PAPILLOMA TITLE OF INVENTION: VIRUS MAIN CAPSIDE PROTEIN AND USE THEREOF
                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/5:
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Abrams, Samuel B.
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 841
TELECOMMUNICATION INFORMATION:
APPLICANT: Cohen, Daniel APPLICANT: Blumenfeld, Ma: APPLICANT: Chumakov, Ilya
                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
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                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (000)
TELEFAX: 66141 PENNIE
TELEX: 66141 PENNIE
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                                                                                                                                                  567 AGAGTTGCCCAAAGTGTTTT 548
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                                                                                                                                                                                                            18;
                                                                                                                                                                       1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Pennie & Edmonds LLP
1155 Avenue of The Americas
                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ethel Michele De Villiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (650) 493-5556
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                    1 .. 660
                                                                                                                                                                                                                                                                                                      Sdo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          York
                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (650) 493-4935
                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                             84.0%; Score 16.8; DB 4; Length 661; 90.0%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/578,634
                        Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8484-007
                                                                                                                                                                                                                   0; Mismatches
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FILE REFERENCE: GENSET.047AUS

OF INVENTION:

Bougueleret, Lydie Bihain, Bernard

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; Sequence 101, Applicat
; Patent No. 6020476
; GENERAL INFORMATION:
APPLICANT: Page, I
                                                                                    US-08-742-185-101
                                                                                                                RESULT 5
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                                                                                                                                                                                                Ś
                                                                                                                                                                                                                                                                                NAME/KEY: misc_binding
/ LOCATION: 1489...1513
/ OTHER INFORMATION: 8-94-252 probe
US-09-539-333D-162
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/162,288
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/416,384
PRIOR FILING DATE: 1999-10-12
     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 162
                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer bind LOCATION: 1651..1669
                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: primer bind LOCATION: 1250...1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 8-94-252.mis2, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 30
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 8-94-252.mis1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1501
OTHER INFORMATION: 8-94-252 : polymorphic base A or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc binding LOCATION: 1482..1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR FILING DATE: 1999-03-30
PRIOR PELICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                local
                                                                                                                                               427 AGAGCTGCCCAAACTGCTTT 408
                                                                                                                                                                        1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                        18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/143,928
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3001
                                                             Application US/08742185
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Page, David C.
Reijo, Renee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EBSSIOUX, LAUTENT
PENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
                                                                                                                                                                                                                                 84.0%;
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                 Score 16.8;
Pred. No. 17
                                                                                                                                                                                                                                       DB 4; Length 3001;
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APPLICANT: KAHAN Leng
APPLICANT: Arthur B. Raitano
APPLICANT: Duglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
FILE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT EILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-323-873A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-742-185-101
                                                                                                                                                                                                                                                                      GENERAL
                                                                                                                                                                                                                                                                             Sequence 1, Application US/09323873A
Patent No. 6329503
UMBER OF SEQ ID NOS:
                                                                                                                                                                                                        APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 01
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: STRANDEDNESS: SIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                       22516 AGAGATTGCCAAACTGTTTT 22535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin PC-1-
                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                          1 AGAGATGCCCAAACTGTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         f: 43795 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (617) 861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.0%; Score 16.8;
90.0%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/310,429
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHI94-07A2
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US-09-323-873A-1
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                                                                                                                                                                                                                                                                                                                                                                                 US-07-903-047-7/c
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09323873A Patent No. 6329503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/07903047 Patent No. 5229285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: STEVE Chappell MICCHell
APPLICANT: STEVE Chappell MICCHEL
APPLICANT: STEVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1195
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Kajiya
APPLICANT: Nakano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3627
                                                                                                                                                                                     APPLICANT: Kajiyama, Naoki
APPLICANT: Nakano, Elichi
TITLE OF INVENTION: Thermostable Luciferase Of Firefly, No. 5229285el Recombi
TITLE OF INVENTION: Thermostable Luciferase Gene Of Firefly, No. 5229285el Recombi
TITLE OF INVENTION: DNA, And Process For The Preparation Of Thermostable
TITLE OF INVENTION: Luciferase Of Firefly
COMPUTER READABLE FORM:
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                    COUNTRY:
                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 GAGAAGCCCAAACTGCTTT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     596 GAGAAGCCCAAACTGCTTT 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                    10036-2711
                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arthur B. Raitano
Douglas C. Saffran
                                                               New York
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                                                                                                      E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.0%; Score 15.8; 89.5%; Pred. No. 42;
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Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; | Length 3627;
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US-07-903-047-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 13, patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1644 harm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,047
FILLING DATE: 19920623
                                                      TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND TITLE OF INVENTION: PROCESS FOR PRODUCING MUTANT-TYPE LUMINESCENT PROTEIN NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,752
                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 711
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,1 REFERENCE/DOCKET NUMBER:
                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MALEK & MOOS ADDRESSEE: P.C. STREET: 1758 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   match
Local Similarity 94.1%; Pred. No. 60;
es 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: ARLINGTON
                                                                                                                                                                                                   FILING DATE: 08-JUL-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AGAGATGCCTAAACTGT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGAGATGCCCAAACTGT 17
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                          703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                     7126-0009-0
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                                                                                                     ; NAME/KEY: CDS
; LOCATION: 1..1644
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-380-061B-15
                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-380-061B-15/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                     Matches
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01026
FILING DATE: 7-APR-1998
APPLICATION NUMBER: GB 9707468.8
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703)816-4000
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHITE, PETER JOHN
LOWE, CHRISTOPHER ROBIN
MURRAY, JAMES AUGUSTUS HENRY
TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SQUIRRELL, DAVID JAMES
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1 AGAGATGCCCAAACTGT 17
                                 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                              NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 12.
                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/380,061B
FILING DATE: 25-Aug-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                               LENGTH: 1644 base pairs
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                                              77.0%; Score 15.4; 94.1%; Pred. No. 60
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                              Mismatches
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                                               60;
                                                          DB 3; Length 1644;
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                                                                                                                                              Sequence 5, Application US/08460934 Patent No. 5814465
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                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,773
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
OF THE OBJECT OF THE OBJEC
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APPLICANT: WOOD, Keith V.
APPLICANT: GRUEBER, Monika G.
TITLE OF INVENTION: MUTANT LUCIFERASES
NUMBER OF SEQUENCES: 16
           APPLICANT:
                                                                              APPLICANT:
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NAME/KEY:
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PILING DATE: 03-JAN-1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: Foley & Lardner
STREET: P.O. Box 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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TYPE: nucleic acid
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REGISTRATION NUMBER: 31,136
REFERENCE/DOCKET NUMBER: 19017/166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                        369 AGAGATGCCTAAACTGT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGAGATGCCCAAACTGT 17
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TATSUMI, HIROKI
FUKUDA, SATOSHI
KIKUCHI, MAMORU
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1..1644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.0%; Score 15.4; 94.1%; Pred. No. 60;
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                                                                                        RESULT 13
US-08-782-118-5/c
Sequence 5, Application US/08782118
Patent No. 5843746
GENERAL INFORMATION:
APPLICANT: TUTSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
FILING DATE: 24-APR-1995
ATTORNEY/ACENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 7126-001-0
                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-413-22-1
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1704 base pairs
LENGTH: 1704 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 05-JU
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                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                   429 AGAGATGCCTAAACTGT 413
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                                                                                                                                                                                                    1 AGAGATGCCCAAACTGT 17
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INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA
INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
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1..1704
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                                                                                                                                                                                                                                                          77.0%; Score 15.4; 94.1%; Pred. No. 60
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                                                                                                                                                                                                                                                                                                                               /note= "Nucleotide sequence of the
biotinylated firefly luciferase gene contained in recombinant
plasmid pHLf203 DNA"
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US-08-782-118-5
                                                                      Matches
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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INFORMATION FOR SEQ ID NO: 5:
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APPLICANT: KOYAMA, YASUJI

TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE

TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNI

TITLE OF INVENTION: FOR BIOTINYLATED BIOTINATED AND A BIOLUMINESCENT

TITLE OF INVENTION: ANALYSIS METHOD
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CORRESPONDENCE ADDRESS:
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FILING DATE: 27-UUL-1994
PRIOR APPLICATION DATA:
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FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                             NAME/KEY: misc feature
IOCATION: 1..1704
OTHER INFORMATION: /note= "Nucleotide sequence of the
OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombinant
OTHER INFORMATION: plasmid pHLf203 DNA"
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                                                                                       Local Similarity
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429 AGAGATGCCTAAACTGT 413
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                                     1 AGAGATGCCCAAACTGT 17
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94.1%;
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                                                                           0; Mismatches
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                                                                                             Score 15.4;
Pred. No. 60
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                                                                                   Gaps
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US-08-460-934-8/c ; Sequence 8, Application US/08460934 ; Patent No. 5814465

RESULT 14

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RESULT 15
US-08-782-118-8/c
; Sequence 8, Application US/08782118
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APPLICATION NUMBER: JP 193798/1994

FILING DATE: 27-UUL-1994

PRIOR APPLICATION NUMBER: JP 54625/1995

FILING DATE: 14-MAR-1995

PRIOR APPLICATION NUMBER: JP 54625/1995

PRIOR APPLICATION NUMBER: JP 98857/1995

PRIOR APPLICATION NUMBER: JP 98857/1995

PILING DATE: 24-APR-1995

PILING DATE: 24-APR-1995
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NAME/KEY:
LOCATION:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: FOR BIOTINYL
TITLE OF INVENTION: FOR BIOT
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,6
REFERENCE/DOCKET NUMBER:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
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TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
                                                                                                                                                                             Local Similarity nes 16; Conserv
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CLASSIFICATION:
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                                                                                                      369 AGAGATGCCTAAACTGT 353
                                                                                                                                        1 AGAGATGCCCAAACTGT 17
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1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                           Conservative
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                                                                                                                                                                                          94.18;
                                                                                                                                                                                                           77.0%;
                                                                                                                                                                                                                                                                                                     /note= "The nucleotide sequence of
the biotinylated firefly luciferase gene contained in
recombinant plasmid pHLf248 DNA"
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FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA,
PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
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                                                                                                                                                                                          Score 15.4;
Pred. No. 6
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                                                                                                                                                                        Mismatches
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US-08-782-118-8
                                                                        Matches
                                                                                                        Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                LOCATION: 1..1908
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JI
FILING DATE: 14-MAR-11
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JI
FILING DATE: 24-APR-1:
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APPLICANT: TATSUM
APPLICANT: FUKUDA
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APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYL
TITLE OF INVENTION: FOR BIOT
TITLE OF INVENTION: PROCESS
TITLE OF INVENTION: ANALYSIS
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER; 71
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                       Local
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                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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FILING DATE: 05-JUN-1995
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
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STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
369 AGAGATGCCTAAACTGT 353
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                                                                                     Similarity
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EDNESS: double
                          AGAGATGCCCAAACTGT 17
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FUKUDA, SATOSHI
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                                                                                77.0%; Score 15.4; 94.1%; Pred. No. 62;
                                                                                                                                                                                                           recombinant plasmid pHLf248
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FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
ANALYSIS METHOD
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## SUMMARIES

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## ALIGNMENTS

REFERENCE AUTHORS TITLE	SOURCE ORGANISM	DEFINITION ACCESSION VERSION	RESULT 1 AX026102
1 Mueller-Schilling,M., Krammer,P. and Oren,M. Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX026102 AX026102 AX026102 AX026102.1 GI:10187533	20 bp DNA linear PAT 16-SEP-2000
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                                    Mueller-Schilling,M., Krammer,P. and Oren,M. Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 28 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)
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                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 28 from Patent DE19847779.
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 20 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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/organism≈"Homo sapiens"
                                  Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AX026092 2827 bp
Sequence 4 from Patent DE19847779.
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                   AX026092
                                                                                                                                                     h 100.0%; Score 20; DB
Similarity 100.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-MAY-1995) F.H. Rudert, Genesis Research & Development, Corporation Ltd., PO Box 50, Auckland, NEW ZEALAND Overlaps with X81335, & X82279-X82286.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identification of a silencer, enhancer, and basal promoter region in the human CD95 (Fas/APO-1) gene DNA Cell Biol. 14 (11), 931-937 (1995)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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546 c 511 g
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
patent: DE 19847779-C 4 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 1 from Patent DE19847779.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                             Sequence 1262 from Patent WO03008583 AX695635
     Homo sapiens
                                                AX695635.1 GI:29418787
                Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
784 c 809 g 84
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676 c 657 g
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100.0%; Pred. No. 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

no Aug 31, 2001 this sequence version replaced gi:14161146.

On Aug 31, 2001 this sequence version replaced from overlapping clones.

During sequence assembly data is compared from overlapping clones which that the together with a note of the overlapping clone name. Note that the variation and the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with corresponding to the corresponding to the overlapping clone, as we submit sequences with corresponding to the sequence with the corresponding to the corresponding to the correspond
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                          http://www.sanger.ac.uk/projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Further information can be found at Mapping Group. Further information can be found at http://www.sanger.ac.uk/NGD/Chr10 Rp11-399019 is from the library RPCI-11.2 constructed by the group of pleter de Jong. For further details see
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                         This sequence is the entire insert of clone RP11-399019 The true left end of clone RP11-496H23 is at 166408 in this sequence. The true right end of clone RP11-30415 is at 18704 in this sequence.
                                                                                                                                http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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/db_xref="taxon:9606"
8836 c 9010 g 140/
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100.0%; Pred. No. 47;
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MZRY, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Aydeji, M., Baca, E., Baden, H., Biswalo, K., Blair, J., Barber, M., Barnsread, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cravez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Charvez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Gerra, M., Goster, M., Guerra, M., Gue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC133743.2 GI:25139560
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/note="Sequence confirmed by AC015461 sequenced by WIBR."

55669 a 36398 c 36888 g 58358 t
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105808. 105972
/note="Sequence from AC015461 sequenced by WIBR."
105973. 105989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 9; Length 187313; 100.0%; Pred. No. 38;
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G IN PROGRESS
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TITLE
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AL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Daylor Plaza, Houston, 7x 77030, USA
The Sequence in this sequence version replaced gi:23096694.
The sequence in this assembly is a combination of BaC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas individual sequence contigs are ordered and oriented, and separated assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul. - L., Puzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Sutton, A., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Tomas, N., Thomas, S., Tingey, A., Trafos, Z., Usmani, K., Wang, O., Wang, S., Warren, R., Walter, B., Wang, J., Walten, R., Walter, R., Wang, J., Walten, R., Willson, R., Wless, R., Wooden, H., Worley, K., Wright, D., Wright, R., Mu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Weinstock, G. and Gibbs, R.A. Smith, D.R., Holt, R.A., Smith, H.O., and A., Smith, H.O., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Center clone name: CH230-182C23

Assembly program: Phrap; version 0.990329

Consensus quality: 18923 bases at least Q40

Consensus quality: 19344 bases at least Q30

Consensus quality: 19344 bases at least Q30

Consensus quality: 195848 bases at least Q30

Estimated insert size: 190572; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                      Center project Information
                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM

    Genome Center
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<sup>\*</sup> NOTE: Estimated insert size may differ from sequence length

\* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 9 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* be preserved. 50225 50325 50224: contig of 50224 bp in length 50324: gap of unknown length 53089: contig of 2765 bp in length

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Page 5
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FEATURES
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Muzny, D. Marie, Metzker, M. Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amini, A., Anguiano, D., Anyal-bechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Barbebechi, V., Aoyagi, A., Ayodeji, M., Barbetad, M., Benahmed, F., Baldwin, D., Bair, J., Barber, M., Barratead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Byth, p., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Byth, p., Brown, M., Brantead, M., Carderon, E., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Chen, Z., Chen,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248752 bp DNA linear HTG 09-MAY-20 Rattus norvegicus clone CH230-4E8, *** SEQUENCING IN PROGRESS *** 3 unordered pieces.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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220275
221474
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203077. .204817
203077. contig"
/note="wgs_contig"
a 38543 c 39231 g
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/mol_type="genomic DNA"
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198830. .199863
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165940. .167729
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223386: gap of unknown length
224587: contig of 1201 bp in length
224687: gap of unknown length
225923: contig of 1236 bp in length
226023: gap of unknown length
227648: contig of 1625 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53189: gap of unknown length 128906: contig of 75717 bp in
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129006: gap of unknown length
220174: contig of 91168 bp in length
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100.0%; Pred. No.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 2; Li; pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g of 1199 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 248752)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas (in the feature table below represents a scaffold in the Atlas (assembly (a 'contig-scaffold'). Within each contig-scaffold, and separated individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAY-2003) Human Genome Sequencing Center, Department Submitted (19-MAY-2003) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Baylor College of Medicine, One of Medi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contex close for formation
Center project name: GATW
Center project name: GT230-48
Center clone name: CH230-48
Center clone name: CH230-48
Consensus quality: 214125 bases at least Q40
Consensus quality: 21412 bases at least Q40
Consensus quality: 21412 bases at least Q20
Estimated insert size: 215006; sum-of-contigs estimation
Consensus quality: CM2523 bases at least Q20
Consensus quality: 21423 bases at least Q20
Consensus quality: 21423 bases at least Q20
Estimated insert size: 215006; sum-of-contigs estimation
Consensus quality: CM2524 bases at least Q20
Consensus quality: 21423 bases at least Q20
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Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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REFERENCE
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AC121457
                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                         ACCESSION
VERSION
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
                                          Rattus.

1 (bases 1 to 264615)

Metzke
                                                              Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                          AC121457.3 GI:23907899
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                      Rattus norvegicus clone CH230-146J5, ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                1 AATGTTGCTTAAGCTTTTT 19
                                                                                                                                                                                                                                                  AC121457
                                                                                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              66997 a 42200 c 42265 g 64973 t 32317 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245924
247300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end_sequence:BH305317"
244828. .245823
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clone_end:Sp6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs contig"
complement (237880)
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91810. .93031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="wgs_contig"
184165. .185672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="wgs_contig"
152801. .154271
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clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="wgs_end_extension
clone_end:T7"
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                                                                                                                                                                                                                                                                                                                                                                      100.0%; Preu. ...
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 19; DB 2; 100.0%; Pred. No. 1.1e+(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence:BH305316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245823: contig of 245823 bp in length 245923: gap of unknown length 247299: contig of 1376 bp in length 247399: gap of unknown length 248752: contig of 1353 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end:Sp6
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                                                                                                                                                                                                                                     264615 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .238728)
                                                                                                                                                                                       DNA linear .... PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                     .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 248752;
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Baldwin, V., Aoyagi, A., Ayodeji, M., Barca, E., Baden, H., Baldwin, V., Barder, H., Baldwin, S., Barder, H., Barder, M., Barnaread, M., Bernantead, M., Bryant, K., Barder, M., Barnaread, M., Baryant, W., Barnaread, M., Baryant, M., Carter, M., Colderon, E., Char, R., Saratt, M., Cher, A., Chun, J., Charley, M., Carter, M., Cox, C., Coyle, M., T., Chen, P., Soura, L., Dayado, J., Charley, M., Carter, M., Cox, C., Coyle, M., T., Chen, P., Soura, L., Dayado, O., Dasta, C., Davy, Carter, M., Dayar, D., Dayado, O., Dasta, C., Davy, C., Ar, Falla, T., Fan, D., Dayado, O., Dasta, C., Davy, C., Bray, Y., Dinh, H., Divyer, M., Dayado, D., Dayado, C., Ar, Falla, T., Fan, D., Dayado, O., Dayado, O., Dayado, C., Bary, Y., Dinh, H., Divyer, M., Dayado, D., Dayado, M., Bartha, M., Dayado, M., Bartha, M., Bartha, M., Bartha, M., Carter, M., Falla, T., Fan, J., Dayado, M., Bartha, M., Bartha, M., Bartha, M., Carter, M., Falla, T., Fan, J., Charley, M., Flagg, M., Sarat, J., Gatay, M., Garrat, M., Harray, Y., Havias, and M., Hanil, C., Hanilton, C., Hanilton, C., Hanilton, M., Bartha, M., Mahladato, M., Martha, M., Mahladato, M., Martha, M., Mahladato, M., Martha, M., Mahladato, M., Martha, M., Mahladato, M., Murph, M., Martha, M., Martha, S., Mangun, B., Martha, M., Martha, S., Mangun, B., Martha, M., Martha, S., Mangun, M., Martha, M., Martha, S., Mangun, M., Martha, M.
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REFERENCE AUTHORS

TITLE

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COMMENT

AUTHORS TITLE JOURNAL

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FEATURES
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RNCCND1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* is not known and their order in this sequence record is

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* because of the sequence of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                            1 AATGTTGCTTAAGCTTTTT 19
                                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                            CCND1 gene; cyclin D1.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                  RNCCND1 1454 bp mRNA
R.norvegicus CCND1 mRNA for cyclin D1.
Bianchi, S., Fabiani, S., Muratori, M., Arnold, A., Sakaguchi, K.
                                                                                                                                                                                          X75207.1 GI:473122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
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Center Clone name: CH230-146J5

Assembly program: Phrap; version 0.990329

Assembly program: Phrap; version 0.990329

Consensus quality: 207625 bases at least Q40

Consensus quality: 211034 bases at least Q30

Consensus quality: 213357 bases at least Q20

Consensus quality: 213357 bases at least Q20

Estimated insert size: 215749; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: GYKE
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enter: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="wgs_contig"
complement(262294. .263119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_contig"
4867. .6350
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1565. .3140
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clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nd sequence:RWBAG51TJB"
42319 c 42274 g 67234 t 49010 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _xref="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%; Score 19; DB 2;
100.0%; Pred. No. 1.1e+
tive 0; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-SEP-1993) M. Brandi, Endocrine Unit, University of Florence, Dept of Clinical Physiopathology, Viale Pieraccini 6, 50139 Firenze, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 204 (2), 691-700 (1994) 95071382
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                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 235 from Patent WO0224865. AX684916
                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (fission yeast)
                                                                                                                                                                                           cluster proteins
Patent: WO 0224865-A 235 28-MAR-2002;
                                                                                                                                                                                                                        Holtzman, D., Madden, K., Maxon, M. and Sherman, A. Modulation of secondary metabolite production by zinc binuclear
                                                                                                                                                                                                                                                                                                                                                                                    AX684916.1 GI:29371356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="CCND1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
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| db_xref="GI:473123"
| db_xref="SWISS-PROT:P39948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="CYCLIN D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="CCND1"
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                                                                  /organism="Schizosaccharomyces pombe"
/mol_type="genomic DNA"
/db_xref="taxon:4896"
1 307 c 323 g 551 t
                                                                                                                                                       Location/Qualifiers
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     92.0%;
95.0%;
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Pred. No. 4.3e+02;
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     Score 18.4; DB 6;
Pred. No. 4.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1454;
                         Length 1689;
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 AATGITGITTAAGCITTTTT 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis, GenomeScan gene prediction, Similarity but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JAN-2003) National Institutes of Health, Mammalian dene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AATGTTGCTTAAGCTTTTTT 20
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Mus musculus, cyclin D1, clone MGC:7003 IMAGE:3155470, mRNA
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         611 a
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                                                 /db_xref="LocusII:12443"
/translation="MEHQLLCCEVETIRRAYPDTNLLNDRVLRAMLKTEETCAPSVSYFKCVQKEIVPSNRKIVATWMLEVCEEQKCEEVFPLAMNYLDRFLSLEFLKKSRLQLLGATCMFVASKMKETIPLTAEKLCIYTDNSIRPEELLQMELLLVNKLKWNLAAMTPHDFIEHFISKMPEADENKQTIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAAMQGLNLG
                         SPNNFLSCYRTTHFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQNVDPKATEEEGE
VEEEAGLACTPTDVRDVDI"
                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="cyclin_D1"
/protein_id="AAH44841.1"
/db_xref="G1:27924089"
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="MGC:7003 IMAGE:3155470"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"/
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                                                                                                                                                                                                                                                                                          "Vector: pCMV-SPORT6"
617 g
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TITLE
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Best Local Similarity
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1440 AATGTTTCTTAAGCTTTTTT 1421
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                                                      19;
                       1 AATGITGCTTAAGCTTTTTT 20
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                                                                                                                                                                                         Novel compositions and methods for cancer Patent: WO 03008583-A 978 30-JAN-2003; Sagres Discovery (US)
                                                                 Similarity
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AATGITGCTTAAGCTTTTT 20
                                                                                                                                                                                                                              Morris, D.W. and Engelhard, E.K.
                                                                                                                                                                                                                                                                                 Mus musculus
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                                                   Conservative
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                                                                                                               /db_xref="taxon:10090"
904 c 988 g
                                                                                                                                        organism="Mus musculus"
/mol_type="genomic DNA"
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                                                              92.0%;
95.0%;
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                                                          Score 18.4; DB 6;
Pred. No. 3.7e+02;
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Search completed: August 1, 2003, 17:32:59 Job time: 84.1573 secs

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## SUMMARIES

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19 19 18.4 18.4	Score
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468 617 159 160	Length I
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## ALIGNMENTS

	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 BH867204 LOCUS DEFINITION
Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mccombie@cshl.org Plate: hg93 row: f column: 08	Unpublished Contact: W. Richard McCombie Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center	1 (bases 1 to 468) Rabinowicz,P.D. O'Shaughnessy,A.L., Balija,V., Dedhia,N., Rabinowicz,P.D., O'Shaughnessy,A.L., Miller,S., Nascimento,L., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., McCombie,W.R. and Martienssen,R.A. Zutavern,T., McCombie,W.R. and Martienssen,R.A.	Zea mays Zea mays Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Vagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Spermatophyta; Magnoliophyta; Liliopsida; Clade; Panicoideae; Andropogoneae; Zea.	BH867204 BH867204.1 GI:22103101 GSS.	468 bp DNA linear GSS 05-AUG-2002 BH867204 MGS-ZmaysF (JM107 adapted methyl filtered) Zea mays genomic clone hg93f08 5', genomic survey sequence.

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Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                             Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnic, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 617)
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                                                                                                                                                                                                                                                                                                                       whitelaw@tigr.org
                                                           /clone="zMMBTa064N04"
/clone=lib="ZM_0.6_1.0_KB"
/clone="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
103 c 113 g 235 t
                                                                                                                                                                           /db_xref="taxon:4577"
                                                                                                                                                                                                 /strain="B73"
                                                                                                                                                                                                                                  organism="Zea mays"
                                                                                                                                                                                                                                                                    ocation/Qualifiers
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/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleofide was
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in Ml3mpl9, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a. "

95 g 175 t
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/clone="hg93f08"
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/cultivar="B73"
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   95.0%; Score 19; DB 29;
100.0%; Pred. No. 1.1e+03;
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+ive 0; Mismatches
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                 DB 29; Length 617;
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S Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai K., K., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., C., Kawai, J., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sujahara, Y., Suzuki, H., Takahashi, F., Tatero, M., Tominaga, N., Tsunoda, Y., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Susaki, Y., RIKEN Mouse ESTs (Konno, H., et al. 1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazak.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Conservative
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                /tissue_type="head"
/dev_stage="0 day neonate"
                                                                                                                 clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                        sex="mixed"
                                                                                                                                                                                                                                                                             clone="4831423J17"
                                                                                                                                                                                                                                                                                                  db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                strain="C57BL/6J"
                                                                                                                                                                       host="DH10B"
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BASE COUNT
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AV174680/c
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Ito 160)

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AV174680 Mus musculus C57BL/6J 8-day embryo Mus musculus CDNA clone
5730411L18, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation for the synthesis of full length cDNA
trehalose and its application for the synthesis of full length cDNA
(proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Science Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from Lambda FLC I."
20 c 29 g
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95.0%;
                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
/dev_stage="8-day embryo"
/clone_lib="Mus musculus C57BL/6J 8-day embryo"
                                                                                                         clone="5730411L18"
                                                                                                                                                                    strain="C57BL/6J"
                                                                                                                                                    xref="taxon:10090"
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AW213875
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                    RESULT 6
AV134425/c
                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 198) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: uo44d03.yl
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AV134425
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                                                                                                                                                  AATGTTTCTTAAGCTTTTTT 52
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_"NCI_CGAP_Lu29"
/clone="Organ: lung; Vector: pcMV-spORT6; Site_1: Sall;
/note="Organ: lung; Vector: pcMV-spORT6; Site_1: Oligo d
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d
Site_1: Sall;
Site_1: Sal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stem cell origin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="IMAGE:2645381"
'tissue type="spontaneous tumor, metastatic to mammary.
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                       213 bp
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                                                                                     AUTTORS
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Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayateu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 226)
                                                                                                                                                                                                             BB834512.1 GI:17012755
                                                                                                                                                                                                                                                  BB834512
226 bp mRNA linear EST 19-1
BB834512 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) cDNA Mus musculus cDNA clone G93003IG12 3', mRNA
                                                                                                                                                          Mus musculus
                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AATGTTGCTTAAGCTTTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akihira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Owa, C., Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Waranabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Okazaki, Y., and Hayashizaki, Y., Yoshino, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@rtc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Science Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="10-11 day embryo"
/clone_lib="Mus musculus C57BL/6J 10-11 day embryo"
22 c 54 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        210
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 237)
Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
                                                                                                                              Mus musculus
                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                    AV133072 237 bp mRNA linear EST 01-JUL
AV133072 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA
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                                                                                                                                                                                                   AV133072.1
                                                                                                                                                                                                                                 clone 2700095E14, mRNA sequence.
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-889 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara, Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          turther details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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The Institute of Physical and Chemical Research (RIKEN)
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/ceil_line="RCB-0527 Jyg-MC(B)"
/clone_lib="RIKEN full-length enriched, mammary gland
RCB-0527 Jyg-MC(B) cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:10090"
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Pred. No. 1.5e+03;
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                             Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci Konno, H., Aizawa, K., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Hirozane, T., Mori, F., Ishii, Y., Ishikawa, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Koya, S., Kurihara, C., Kusakabe, M. Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Kiyosawa, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Salto, K., Shibata, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toyano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, N., Matamabe, S., Yamamaura, T., Yamanatsu, M., and Hayashizaki, Y., Natamatsu, M., and Hayashizaki, Y., Natamatsu, M., and Hayashizaki, Y., Matamatsu, M., and Hayashizaki, Y., and M., and Hayashizaki, Y., and Matamatsu, M., and Hayashizaki, Y., and M., and 
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Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of full length cDNA
trehalose and its application for the synthesis of full length cDNA
trehalose and its application for the synthesis of full length cDNA
(proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
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Tel: 81-298-36-9145
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BB048825 RIKEN full-length enriched, adult male olfactory bulb Mus
musculus cDNA clone 6430596J05 3' similar to S78355 Cyl-lecyclin D1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/strain="C57BL/6J"
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DEFINITION RESULT 10 BB546588/C

, mRNA sequence.

BB546588 RIKEN full-length enriched, 0 day neonate eyeball Mus musculus cDNA clone E130310020 3' similar to S78355 Cyl-1=cyclin D1

linear

EST 31-JUL-2000

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COMMENT
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URL:http://genome.gsc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
Carninci, P., Nishiyama, Y., Shibata, Y., Sasaki
Tohan, Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Toh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical Research (RIKEN)
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Fax: 81-45-503-9216
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Carninci,P. and Hayashizaki,Y. Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
233 AATGTTTCTTAAGCTTTTTT 214
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/dev_stage="adult"
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URL:http://genome.gsc.riken.go.jp/
Carninci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
V., N., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/lab_host="DH10B"
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/clone="E130310020"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lib="RIKEN full-length enriched, 0 day neonate
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BI289904/c
                        RESULT 12
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                                                                                                                                                                                                                 ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                      Local Similarity
                                                                                         1 AATGTTGCTTAAGCTTTTTT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
                                                           AATGTTTCTTAAGCTTTTTT 246
                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akhira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Shibata, Y., Shigemoto, Y., Niisuma, H., Oda, H., Owa, C., Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Sugahara Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Okazaki, Y. and Hayashizaki, Y., Yoshino, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 AATGTTTCTTAAGCTTTTTT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Butheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV135706 Mus musculus C57BL/6J 10-11 day embryo Mus musculus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV135706.1 GI:5321436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone 2810020K08, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                   Conservative
                                                                                                                                                                                                                             88
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                                                                                                                                                                                                    /dev_stage="10-11 day embryo"
/clone_lib="Mus musculus C57BL/6J 10-11 day embryo"
34 c 61 g 87 t
                                                                                                                                                                                                                                                                                      /clone="2810020K08"
                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                          sex="mixed"
                                                                                                                                                                                                                                                                                                                        strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chie Owa
                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                              92.0%;
95.0%;
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                                                                                                                                 0
                                                                                                                                       Score 18.4; DB 9;
Pred. No. 1.6e+03;
                                                                                                                                                  Length 270;
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BI289904

278 bp

mRNA

EST 19-JUL-2001

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VERSION
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MEDLINE
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Email: herre -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UI-R-DK0-cfp-f-04-0-UI.s1 UI-R-DK0 Rattus norvegicus cDNA clone UI-R-DK0-cfp-f-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI289904.1 GI:14947954
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Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8889548
Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 278)
/Clone_inb="U1-K-DKO"
//otce="Vector: pT/T3D-Pac (Pharmacia) with a modified
/notce="Vector: pT/T3D-Pac (Pharmacia) with a modified
/notce="Vector: pT/T3D-Pac (Pharmacia)
library is a subtracted library derived from a mixture of
five individually tagged normalized rat libraries:
five individually tagged normalized rat libraries:
brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP (20%),
aorta-nRAP (20%), and placenta-nRPP (20%). Each original
library was constructed from a mixture of equal amounts of
RNA from seven different developmental time-points:
embryonic day 17, embryonic day 19, embryonic day 21,
adult day 1, adult day 12, adult day 75, and adult day
200. (Exception: the aorta pool does not contain embryonic
day 17 RNA and the placenta pool contains only the three
embryonic stages). Each library was normalized
individually according to the procedure described by
Bonaldo, Lennon & Soares (Genome, Research Genome 6:
791-806, 1996). For construction of the DKO subtracted
library, plasmid DNA from each of the five individually
tagged normalized libraries was mixed in the proportions
specified above and electroporated into competent bacteria
for production of single-stranded circular DNA
representing the pool of libraries. Single-stranded
circular DNA representing these five normalized libraries
was then used as a tracer in a subtractive hybridization
with a driver (PCR amplified inserts from a plasmid DNA
template preparation) comprising; a) a set of about 1,000
arrayed clones from each of the five non-normalized
libraries of brain (CTOs), heart (CXOs), The resulting pool of
approximately 5,000 clones represented about 33.3 of the
final driver population. A set of about 10,000 clones
placenta (CXO). The resulting pool of about 10,000 clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
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/clone="UI-R-DK0-cfp-f-04-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _type="mRNA"
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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                FEATURES
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Best Local (
                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya,
T., Tsunoda, Y., Watahiki, A., Watahabe, S., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramateu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB049315 RIKEN full-length enriched, adult male cerebellum Mus musculus cDNA clone 6530404H10 3' similar to S78355 Cyl-1=cyclin D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AATGTTGCTTAAGCTTTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                   Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carrinci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN Mouse ESTs (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 280)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
                                                                                                                                                                                further details.
                                                                                                                                                                                                                                                19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                             visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_SEQ=None found"
1 41 c 58 g
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/strāin="C57BL/6J"
/db_xref="taxon:10090"
                                                                                      organism="Mus musculus"
                                                                                                                                             Location/Qualifiers
                                                   mol_type="mRNA"
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Pred. No. 1.6e+03;
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clone="6530404H10"

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JOURNAL COMMENT
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Matches 19
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                                                                                                                                                         source
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                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished Other_ESTs: uz82b07.y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 283)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                   Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                          MGI:1436309
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                         image.llnl.gov/image/html/iresources.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:3675541"
/tissue="type="spontaneous tumor, metastatic to mammary.
                                                                               /strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGACTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                            organism≃"Mus musculus"
                                                                                                                                                                           Location/Qualifiers
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cerebellum"
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/lab_host="DH10B"
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                                                                                                        type="mRNA"
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Pred. No. 1.6e+03;
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VERSION KEYWORDS

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1 (base's 1 to 298)

1 (base's 1 to 298)

1 (Sonno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fikuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Wattahiki, A., Wattanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Wattanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., RIKEN Mouse ESTs (Konno, H., et al. 1999)
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                    Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Iaawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV219191 RIKEN full-length enriched, 12 days embryo head Mus musculus cDNA clone 3010086E05 3' similar to 578355 Cyl-1=cyclin D1 (mice, BALB/c, brain, mRNA, 3737 nt), mRNA sequence.
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                                                                                                                            further details.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                               visit our web site (http://genome.rtc.riken.go.jp) for
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 57 c 40 g 99 t
/organism="Mus musculus"
/mol_type="mRNA"
                                                                                          Location/Qualifiers
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                        Score
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ng fragment #2. ptosis-modulation; apoptosis-modulating	Human osteoblast d Human cDNA differe Human cDNA differe Human cDNA differe CDNA encoding SRT Arabidopsis thalia Drosophila melanog Human neuregullin-l Human neuregullin-l Human immune/haema Human polynucleoti CDNA encoding SRT Gene #2812 used to Thyroid cancer rel Arabidopsis thalia

Claim 2; Fig 5; 12pp; German.

This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a

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ABN79875/c
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         The invention relates to improving the production of a secondary metabolite by a fungus. This involves modulating the expression of at least one ZBC (zinc binuclear cluster protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g. antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, a fungal toxin, a modulator of cell surface receptor signalling, a plant
growth regulator, a pigment, an insecticide, or an antineoplastic
                                                                                                                                                                                                                      New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene
                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                             P-PSDB; ABP35686.
                                                                                                                                                                                                                                                                                                                                        Holtzman D,
                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2000; 2000US-233564P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; cell surface receptor; plant growth regulator; pigment;
                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROBIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-2001; 2001WO-US29288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insecticide; antineoplastic; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN79875 standard; DNA; 1689 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fungal ZBC gene sequence #112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN79875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment of the human CD95 receptor promoter which is capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                          2002-352005/38.
                                                                                                                                                                             2; SEQ ID 235; 49pp + sequence listing; English.
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Query Match

Sequence 514 BP; 129 A; 111 C; 118 G; 152 T; 4 other;

84.0%;

Score 16.8;

DB 22;

Length 514;

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RESULT 3
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Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding human SRT proteins. The cDNA sequences are isolated from various different human tissue cDNA libraries. The invention relates to a method for detecting cDNA encoding an SRT protein, a vector containing cDNA polypeptide, and an antibody which binds to SRT. The polynucleotide production of SRT penetrapy and is useful in the recombinant libraries to isolate cDNAs with sequence can be used in gene therapy and is useful in the recombinant libraries to isolate cDNAs with sequence identity to SRT polypeptides, as a hybridisation probe to screen map the gene encoding the SRT polypeptides and analysing genetic polynucleotide sequences can be used in polymerase chain reaction, screening for new therapeutic molecules and generation of antisense RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                            Claim 2; Fig 86; 663pp; English.
                                                                                                                                                                                                                                                                                   New isolated nucleic acid molecule encoding a SRT polypeptide is useful for production of recombinant SRT polypeptides, gene mapping, diagnosing genetic disorders and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-112729/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-2000; 2000WO-US20006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200107611-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; SRT; gene therapy; gene mapping; tissue typing; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Small intestine tissue cDNA encoding SRT protein SEQ ID 86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF93265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF93265 standard; cDNA; 514 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compound. The method results in a decrease in fermentor run-time, a decrease in the size of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the biomass required for the production, which translates into decreased in records ABN79764-ABN79911 represent ZBC genes of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1689 BP; 508 A; 307 C; 323 G; 551 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 AATGTTGTTTAAGCTTTTTT 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0145701.
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                                                                                                                                                                                                                                                                                                                                                                                                      Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55kD i-antigen nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ichthyophthirius multifiliis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immobilisation antigen; i-antigen; ichthyophthiriasis; vaccine; ds; white spot disease; freshwater fish; immune response; infection control.
                                                                                                                                                                                    This invention relates to novel i-antigen polypeptide sequences. I-antigens or immobilisation antigens ar common to a variety of hymenostomatid ciliates and their expression varies in response to hymenostomatid stimuli. This invention relates to i-antigens in rehthyophthirius multifiliis, a protozoan which is an obligate parasite of freshwater fish causing ichthyophthiriasis or white spot disease. The of freshwater fish causing ichthyophthiriasis or white spot disease. The invention includes two polypeptide and polynucleotide sequences for two i-antigens, of 48 and 55 kD. Also included in the invention are antigens, of 48 and 55 kD. Also included in the invention are for identifying I. multifilias serotypes using the nucleotide sequences. A composition (containing the i-antigen nucleotide) capable of eliciting an immune response in fish is useful for prophylaxis, treatment or for controlling I. multifilis infection in fish. Polynucleotide or protein removie of the committed or protein controlled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-1999;
02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000WO-US02962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-506071/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel i-antigen polypeptides and polynucleotides from Ichthyophthirius multifiliis, useful for prophylaxis and treatment of Ichthyophthirius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAR-1999;
                                    vaccines comprising a portion of the amplified product encoding an antigenic i-antigen polypeptide obtained is also useful for treating or antigenic i-antigen polypeptide obtained is also useful for treating or antigenic i-antigen polypeptide obtained is also useful for treating or antigenic in the infection in fish. Sequences AAA97043-A97042, and AAA97066, AAA97065 and AAA97089 represent i-antigen genes and gene fragments identified in the invention. Sequences AAA97043-A97064 (excluding AAA97060) and AAA97071-A97088 represent primers used in the isolation of the i-antigen gene sequences. Sequences AAB25859-B25889 and AAB25893-B25906 represent i-antigen protein and peptide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Figure 3; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection in fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGTTGCTGAAGCTTTTCT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DICKERSON H W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dickerson HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0118634.
99US-0122372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0131121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5.6e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sequence 1404 BP; 447 A; 240 C; 257 G; 460 T; 0 other;

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RESULT 5
AAA52136
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA52136 standard; DNA; 1404 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BTU1; beta-tubulin; protein expression system; negative selection; paclitaxel sensitivity; cell surface; antigen; protozoa; ciliate; live vaccine; Ichthyophthilus multifiliis; immobilization-antigen; live vaccine; Ichthyophthilus multifiliis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 kDa i-antigen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2000
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            Tetrahymena thermophila expresses two major beta-tubulin genes (BTU1 and BTU2), which encode identical beta-tubulin proteins. Either of these two genes (but not both at once) can be disrupted without a detectable change in the cell phenotype. A K350L substitution in the BTU1 beta-tubulin protein confers increased resistance to microtubule-depolymerizing drugs and increased sensitivity to paclitaxel, a microtubule-stabilizing drugs and increased sensitivity to paclitaxel, a microtubule-stabilizing drugs and increased sensitivity of paclitaxel, a microtubule-stabilizing drugs and increased sensitivity to paclitaxel, a microtubule-stabilizing drugs and increased sensitivity to paclitaxel, a microtubule stabilizing drugs and increased sensitivity of selection. Where replacement of Btu1-1K350M with a wild-type BTU1 gene fragment, eliminating the need to incorporate a means for positive selection. Where the host organism is not a T. thermophila mutant containing the Btu1-1K350M allele, BTU1::neol construct, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200046381-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ichthyophthiius multifiliis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i-antigen; freshwater; fish; protozoacide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000WO-US02966.
                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant expression systems for expressing heterologous nucleic acids and producing recombinant protein, comprises nonpathogenic protozoa such as Tetrahymena resistant to paclitaxel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaertig J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3B; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-1999;
substitutes the coding region of the neol gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CLAR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY97177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DICKERSON H W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAERTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dickerson HW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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99US-0124905.
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/codon= (seq:"TAA", aa:Gln)
/product= 55_kDa_i-antigen
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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parmomycin) for that of BTU1, can be used to generate BTU1 gene knockouts and for positive selection. Heterologous nucleic acids (especially encoding antigenic polypeptides) can be inserted into a BTU gene for successful cell-surface expression that is maintained by way of negative selection. Preferred expression vectors disrupt the Btu1-IK350M gene by acid, thereby restoring resistance to paclitaxel in the resulting acid, thereby restoring resistance to paclitaxel in the resulting for stimulating an immune response in a vertebrate. The transgenic protozoan host cells are also useful for producing polyclonal antibodies multifilis immobilization-antigen (1-antigen) protein on their surface infection by I multifilis immobilization-antigen (1-antigen) protein on their surface infection by I multifilis.
infection by I. multifiliis.
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გვგვგვგვგვგგგგგ Sequence 1404 BP; 447 A; 241 C; 256 G; 460 T; 0 other; Local Similarity 84.0%; 90.0%; Score 16.8; DB 21 Pred. No. 5.5e+02; Length 1404;

ş 661 AATGTTGCTTAAGCTACTTT 680 1 AATGTTGCTTAAGCTTTTTT 20

Matches

18;

Conservative

0

Mismatches

2; Indels

**;** Gaps

0

AAA97060 standard; DNA; 1410 BP

AAA97060;

18-DEC-2000 (first entry)

55kD i-antigen coding region.

Immobilisation antigen; i-antigen; ichthyophthiriasis; vaccine; white spot disease; freshwater fish; immune response; infection

Ichthyophthirius multifiliis

WO200046373-AL

10-AUG-2000.

04-FEB-2000; 2000WO-US02962.

04-FEB-1999; 02-MAR-1999; 17-MAR-1999; 99US-0118634. 99US-0122372.

27-APR-1999; 99US-0124905.

(UYGE-) UNIV GEORGIA RES FOUND INC.

LIN T CORNELL RI DICKERSON H W. RES FOUND INC

Dickerson HW,

WPI; 2000-506071/45.

Novel i-antigen polypeptides and polymucleotides from Ichthyophthirius multifiliis, useful for prophylaxis and treatment of Ichthyophthirius infection in figh

Disclosure; Figure 2; 144pp; English

environmental stimuli. This invention relates to i-ant Ichthyophthirius multifillis, a protozoan which is an This invention relates to novel i-antigen polypeptide sequences. J-antigens or immobilisation antigens ar common to a variety of hymenostomatid ciliates and their expression varies in response to environmental stimuli. This invention relates to i-antigens in obligate parasite

> ភិក្ខុសិក្ខិសិក្ខិសិក្ខិសិក្ខិសិក្ខិសិក្ខិសិក្ខិសិក្ខិ of freshwater fish causing ichthyophthiriasis or white spot disease. The cinvention includes two polypeptide and polymucleotide sequences for two i-antigens, of 48 and 55 kD. Also included in the invention are cantibodies capable of binding to the nucleotide sequences and a method for identifying I multifiliis scrotypes using the nucleotide sequences. Composition (containing the i-antigen nucleotide) capable of eliciting controlling I multifiliis infection in fish. Polymucleotide or protein controlling I multifiliis infection in fish. Polymucleotide or protein controlling I multifiliis infection in fish. Polymucleotide or protein cantigen polypeptide obtained is also useful for treating or controlling I multifiliis infection in fish. Sequences AAA97042, and AAA97065, AAA97065 and AAA97080 represent i-antigen genes and gene (excluding AAA9706) and AAA97071-A97088 represent primers used in the i-antigen gene sequences. Sequences AAA97043-A97064 consolution of the i-antigen gene sequences. Sequences AAA97089-B25889 and capable of the i-antigen gene sequences. Sequences AAB2589-B25889 and capable of the i-antigen gene sequences.

Sequence 1410 BP; 449 A; 240 C; 259 G; 462 T; 0 other;

밁 Query Match Best Local ( Matches Local 661 AATGTTGCTTAAGCTACTTT 680 18; 1 AATGTTGCTTAAGCTTTTT 20 Similarity Conservative 90.0%; 0; Mismatches Score 16.8; Pred. No. 5. 5.5e+02 DB 21; Length 1410; o ; Gaps

0

RESULT 7

ABL14642/c

ABL14642 standard; cDNA; 4839 BP.

ABL14642;

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 38408

pharmaceutical; gene; ss. Drosophila; developmental biology; cell signalling; insecticide;

Drosophila melanogaster.

WO200171042-A2

23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.

(PEKE ) PE CORP NY.

Venter JC, Adams M, Li PWD, Myers EW;

P-PSDB; ABB70539 2001-656860/75.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel

Claim 1; SEQ ID NO 38408; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins 18

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RESULT 6
ABT10146/c
ABT10146/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                              The present invention relates to methods of diagnosing breast cancer in a patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867.

ABT1112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients progression, and in monitoring treatment of breast cancer that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction of identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; breast specific gene; breast cancer; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human breast cancer associated coding sequence SEQ ID NO: 280.
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25-APR-2001; 2001US-286090P.
23-MAY-2001; 2001US-292517P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing breast cancer in a patient comprises detecting the level of gene expression in cell or tissue samples, where a differential gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 280; 260pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression is indicative of breast cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                   Sequence 140167 BP; 45038 A; 27502 C; 26800 G; 40827 T; 0 other;
                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2454 AATGTTTCTTAAGTTTTTTT 2435
                                                                                                                                                                                  ftp.wipo.int/pub.published_pct_sequences.
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                                 Similarity
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      Conservative
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90.0%; Pred. No. 5.
                             84.0%; Score 16.8; DB 24; Length 140167; 90.0%; Pred. No. 5.2e+02;
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             Mismatches
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human osteoblast differentiation related cDNA SEQ ID NO 105.
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                                                                                                                                                                                                                                                                                                                                                                                                     (a) screening modulators of precursor stem cell differentiation into osteoblasts, or bone tissue deposition;
(b) diagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporosis; or (c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition.

monitoring the progression of bone tissue deposition.

specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteodystrophy, osteoporosis or male osteoporosis, osteodystrophy, osteodystrophy, osteoporosis, osteodystrophy, os
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2001; 2001US-285691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 105; 78pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-557663/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mertz L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to genes and their expression profiles are used
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                                                                                                                                                                                                                 Sequence 154902 BP; 43917 A; 31458 C; 32848 G; 46679 T; 0 other;
                                                                                                                                                                                                                                                                                                   Panconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
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96683 AATGTTGCTGAAGCTATTTT 96702
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                                                       1 AATGTTGCTTAAGCTTTTT 20
                                                                                                                                          Similarity
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                                                                                                                  Conservative
                                                                                                                                          84.0%; Score 16.8; DB 24; Length 154902; 90.0%; Pred. No. 5.2e+02;
                                                                                                                  0; Mismatches
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                                                                                                                           Indels
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                                                                                                                                 Gaps
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CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (CDA), considered to an expression level in an unactivated (CCDA) to included are modulating (M2) GA by contacting GC with an agent capable of modulating GCA or an inflammation (especially CCC chronic) in a tissue, an allergic response in a subject, exposure of a gene expression profile; (3) detecting (M4) an inflammation (especially CCC subject to a pathogen or sterile inflammatory disease, by detecting the CCC chronic) in a tissue, an allergic response in a subject, exposure of a gene expression profile; (3) detecting (M4) an inflammation (especially CCC subject to a pathogen or sterile inflammatory disease, by detecting the CCC entonic) in a tissue, an allergic response in a subject, exposure of a CCC level of expression in a sample of the tissue of gene(s) from Gs, where CCC (4) treating (M5) an inflammation (especially chronic) or in a tissue, or sterile inflammatory disease, by detecting the CCC risponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having CCC an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having CCC inflammation with an agent that modulates the expression of gene(s) cCC detecting an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile considerably in an inflammation in a tissue; Ms is useful for confile the considerable of modulating considerable considerable considerable considerable considerable considera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 31; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beazer-Barclay Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2000; 2000US-237189P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA differentially expressed in granulocytic cells #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK83460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK83460 standard; cDNA; 165199 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ss; granulocytic cell; DNA chip; bacterial infection; infection; parasitic infection; protozoal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weissman SM, Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vockley J;
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The invention relates to 1046 novel nucleic acids which are used as CC markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when CC they are shown to express one of the 242 sensitivity markers or the CC in the treatment of cancer cell growth in an individual. The markers CC in the treatment of cancer cell growth in an individual. The markers CC can be used as targets in developing anti-cancer agents such as CC developing treatments for cancer, particularly those cancers which CC display resistance to agents and exhibit expression of the markers. The CC cancer agents developed by the novel method can be used to treat CC cancer. Probes based on the markers can be used to treat CC cancer. Probes based on the markers can be used to detect transcripts or CC cells or tissues which mis-express the protein. Cancers which mis-express the protein. Cancers which markers can be used to treat CC cells or tissues which mis-express the protein. Cancers which markers can cell carcinoma), immakana cle.g. fibrosarcoma) leukaemia (e.g. squamous cell carcinoma), and contains and cle.g. squamous cell carcinoma), and contains and contains and cle.g. squamous cell carcinoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
AAS60064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 107; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      Nove1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-602933/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-APR-2000; 2000US-197538P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-2001; 2001WO-US12132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma; squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200179556-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer agent-sensitive marker #65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS60064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS60064 standard; cDNA; 333 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 165199 BP; 48510 A; 33223 C; 34406 G; 49060 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parasitic infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid, used as a marker to TAXOL to treat cancer cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AATGTTGCTTAAGCTTTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bolt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Huffel C;
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                                                                                                                                                                                                                                                                                                                                                                                         determine the effectiveness of in individuals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 24;
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reticulum cell sarcomā, Hodgkin's disease and

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                              δ
                                                                 Query Match
Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 333 BP; 79 A; 63 C; 74 G; 93 T; 24 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA encoding SRT protein isolated from MCF-7 cells SEQ ID 508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF93687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF93687 standard; cDNA; 564 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-2001 (first entry)
                                                                                                                                                                                Sequences AAF93180 - AAF93743 represent polymucleotide sequences encoding human SRT proteins. The cDNA sequences are isolated from various different human tissue cDNA libraries. The invention relates to a method different human tissue cDNA libraries. The invention relates to a method for detecting cDNA encoding an SRT protein, a vector containing cDNA encoding SRT, a host cell transformed with the vector, an isolated SRT encoding SRT, and an antibody which binds to SRT. The polymucleotide polypeptide, and an antibody which binds to SRT. The polymucleotide sequence can be used in gene therapy and is useful in the recombinant sequence of SRT polypeptides, as a hybridisation probe to screen production of SRT polypeptides, as a hybridisation probe to screen libraries to isolate cDNAs with sequence identity to SRT polypeptides, to libraries to isolate cDNAs with sequence identity to SRT polypeptides, to libraries to isolate cDNAs with sequence identity to SRT polypeptides, to map the gene encoding the SRT polypeptides and analysing genetic disorders, tissue typing and disease tissue detection. The SRT polypeptides can be used in polymerase chain reaction, screening for new therapeutic molecules and generation of antisense RNA and RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1999; 99US-0145701.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule encoding a SRT polypeptide is useful for production of recombinant SRT polypeptides, gene mapping, diagnosing genetic disorders and for gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-2000; 2000WO-US20006.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 508; 663pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baker KP, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112729/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                     Sequence 564 BP; 143 A; 121 C; 126 G; 170 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                        and DNA.
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 128
                                                                     17;
                                                                                      Similarity
                      ATGTTGCTTAAGCTTTTTT 20
 ATGTTGCTGAAGCTTTTNT 146
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                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%; Score 16.4; DB 22; Length 333; 85.0%; Pred. No. 8.3e+02;
                                                                                      82.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood WI;
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                                                                                      Score 16.4; DB 22; Length 564; Pred. No. 8.2e+02;
                                                                         0; Mismatches
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                                                                                  Gaps
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RESULT 13
AAC54576
AAC54576 standard; DNA; 1404 BP.
                                                                                                                                                                                                                                                                                                                                                                                                             metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 78358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000.
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05-MAR-1999;
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                                                                                                                               20-MAY-1999;
21-MAY-1999;
                                                                                                                                             19-MAY-1999;
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                                                                                                                                                                          99US-0134256.
99US-0134218.
99US-0134219.
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99US-0132407.
99US-0139452.
99US-0139453.
99US-0139492.
99US-0139454.
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99US-0139457.
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99US-0132486.
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                                                                                                                                 99US-0135353.
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                                               99US-0139119
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RESULT 14
ABL17270
ID ABL17
XX
AC ABL17
XX
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Best Local Similarity
Matches 17; Conserv
               ABL17270;
                                          ABL17270 standard; DNA; 2613 BP.
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15-SEP-1999
15-SEP-1999
20-SEP-1999
20-SEP-1999
21-SEP-1999
22-SEP-1999
24-SEP-1999
25-SEP-1999
26-OCT-1999
06-OCT-1999
06-OCT-1999
07-OCT-1999
07-OCT
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28-OCT-1999;
29-OCT-1999;
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20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
01-SEP-1999;
                                                                                                                                          520
                                                                                                                                3 IGTIGCTTAAGCTTTTTT 20
|||||||||
20 IGTIGCTTAAGTTTTTTT 53.
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                           99US-0149723.
99US-0149929.
99US-0149929.
99US-0149929.
99US-0150566.
99US-0151065.
99US-0151066.
99US-0151438.
99US-0151303.
99US-0151303.
99US-0151303.
99US-0153758.
99US-0154018.
99US-0155406.
99US-0155403.
99US-0155403.
99US-0155403.
99US-0155403.
99US-0155465.
99US-0155465.
99US-0155465.
99US-0156458.
99US-0156458.
99US-0158029.
99US-0158029.
99US-0158029.
99US-0158039.
99US-0159331.
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99US-0159331.
99US-0160767.
99US-0160768.
99US-0160767.
99US-0160768.
99US-0160768.
99US-0160769.
99US-0160814.
99US-0161406.
99US-0161361.
99US-0161361.
                                                                                                                                                                                                                         82.0%;
                                                                                                                                                                                                  Score 16.4; DB 21;
Pred. No. 8.2e+02;
0; Mismatches 1;
                                                                                                                                    537
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                  Length 1404;
                                                                                                                                                                                                0;
                                                                                                                                                                                              Gaps
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20-JUL-1999; 20-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999;

99US-0139458.
99US-0139461.
99US-0139462.
99US-0139462.
99US-0139463.
99US-0139763.
99US-014939.
99US-0140353.
99US-0140353.
99US-0140353.
99US-0140363.
99US-0141287.
99US-0141288.
99US-0141288.
99US-014128.
99US-

18-JUN-1999
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28-JUL-199)
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02-AUG-1999
03-AUG-1999
04-AUG-1999
05-AUG-1999
06-AUG-1999
06-AUG-1999
11-AUG-1999

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RESULT 15
ABL22326
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABJ30511), expressed DNA discloses genomic DNA sequences (ABL16176-ABJ30511),
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2613 BP; 874 A; 462 C; 460 G; 817 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 3283; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ ID NO 18451.
                                                                                                                                                                                                                                                   ABL22326 standard; DNA; 3945 BP
                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                         ABL22326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABB57737-ABB72072)
23-MAR-2001; 2001WO-US09231.
                               27-SEP-2001
                                                           WO200171042-A2
                                                                                     Drosophila melanogaster.
                                                                                                                   pharmaceutical; gene; ds.
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                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   82.0%; Score 16.4; DB 23; Length 2613; 94.4%; Pred. No. 8.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 18451; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                           Sequence 3945 BP; 1117 A; 835 C; 876 G; 1117 T; 0 other;
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                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                Local
2533 TGTTGCTAAAGCTTTTT 2550
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                                                                                Similarity
                                                                 Conservative
                                                                                82.0%; Score 16.4; DB 23; 94.4%; Pred. No. 8.1e+02;
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Search completed: August 1, 2003, 13:55:21 Job time : 10.6987 secs

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Copyright (c) 1993 - 2003 Compug
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13 US-10-027-632-72944

US-10-027-632-9152

US-10-027-632-250885

US-10-027-632-250886

13 US-10-027-632-250886

10 US-09-834-975-65|

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11 US-10-066-543-2878

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13 US-10-027-632-135562
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US-09-834-291-20
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7955.924 Million cell updates/sec
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                                      Sequence 14, Appl
Sequence 20, Appl
Sequence 28, Appl
Sequence 4, Appli
Sequence 1, Appli
Sequence 36459, A
Sequence 69220, A
Sequence 72944, A
Sequence 9152, Appl
Sequence 9152, Appl
Sequence 250886,
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Sequence 250886,
Sequence 2878, Ap
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Sequence 32622, A Sequence 32623, A	Sequence 237203,	Sequence 237202,	-	233945,	Sequence 211911,	Sequence 211910,	Sequence 2901/2,	Sequence 200451,	Sequence 200450,	Sequence 44920, A	281	Sequence 148, App	Sequence 283756,	Sequence 267598,	Sequence 40, Appl	Sequence 3, Appli	Sequence 3866, Ap	Sequence 278366,		æ	_		32	Sequence 157839,

## ALIGNMENTS

US-09-834-291-14

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Sequence 14, Application US/09834291

Patent No. US20020042064A1
                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                           ; ORGANISM: Homo Sapiens US-09-834-291-14
                                                       RESULT 2
US-09-834-291-20
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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
                                                                                                                                                                                                                                                                                                                                SEQ ID NO 14
LENGTH: 20
Sequence 20, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION:
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                      Local
                                                                                                                                                         1 AATGTTGCTTAAGCTTTTTT 20
                                                                                                                                                                                                        20; Conservative
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                                                                                                                                 AATGTTGCTTAAGCTTTTTT 20
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APPLICANT: Krammer, Peter

APPLICANT: Muller-Schilling, Martina

Oren, Moshe

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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: D53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
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                                                                                                                                            Sequence 4, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application UPatent No. US20020042064A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: p53 Binding Areas FILE REFERENCE: 4121-122 CURRENT APPLICATION NUMBER: US/09/834,291 CURRENT FILING DATE: 2001-08-21
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 40
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                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB 100.0%; Pred. No. 18;
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PRIOR PELLUNG DATE: 2000-07-12
PRIOR PELLUNG DATE: 2000-07-12
PRIOR PELLUNG DATE: 2000-07-12
PRIOR PELLUNG DATE: 2000-04-20
PRIOR PELLUNG DATE: 2000-04-20
PRIOR PELLUNG DATE: 2000-03-29
PRIOR PELLUNG DATE: 2000-03-29
PRIOR PELLUNG DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR PELLUNG DATE: 2000-02-24
PRIOR PELLUNG DATE: 1999-11-23
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US-10-027-632-36459/c
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                                                                                                                                                                                                Sequence 36459, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
DBTOD RODITORITON WINDER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-1
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CURRENT FILING DATE: 2001.08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR PLING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
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Patent No. US20020042064A1
GENERAL INFORMATION:
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SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
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US-10-027-632-69220
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 69220
LENGTH: 591
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                        Sequence 15, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     Matches
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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                  APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERBNCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
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94.7%;
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94.7%;
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Pred. No. 3.
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: ECT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 15
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR TILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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GENERAL INFORMATION
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72944
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                    Query Match
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(553)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                           Local Similarity
les 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1999-09-28
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38 AATATTGCTGAAGCTTTTT 19
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                                      1 AATGITGCTTAAGCTTTTTT 20
                                                                               Conservative
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Pred. No. 3.
                                                                                   0; Mismatches
                                                                                                     Score 16.8; DB 13;
Pred. No. 6e+02;
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RESULT 10 US-10-027-632-9152/c

Sequence 9152, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

Application US/10027632

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                                                                                                                                                                   ; ORGANISM: Human
US-10-027-632-250885
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US-10-027-632-250885/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/20,063
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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                                                                                       Matches
                                                                                                                           Query Match
                                                                                                                                                                                                                                                             SEQ ID NO 250885
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SEQ ID NO 9152
LENGTH: 980
                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local (
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28 PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                          ENGTH: 1055
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                                                                                                ocal Similarity
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1 AATGTTGCTTAAGCTTTTTT 20
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                                                                              18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                              84.0%;
90.0%;
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90.0%;
                                                                           0; Mismatches
                                                                                                Score 16.8;
Pred. No. 6.
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                                                                                            6.5e+02
                                                                                                            DB 13; Length 1055;
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(333)
OTHER INFORMATION: n = A,T,C or
US-09-834-975-65
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US-10-027-632-250886
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Patent No. US20020110815A1
GENERAL INFORMATION:
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US-10-027-632-250886/c
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                                                                                                                                                                                      SEQ ID NO 65
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PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE. FRACE.
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APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Bolt, Andrew
APPLICANT: Van Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, P
TILE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
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GENERAL INFORMATION:
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PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                            TYPE: DNA
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                              ENGTH:
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Pred. No. 6.5e+02;
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Query Match

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 1999-10-2-34
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
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TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2878
LENGTH: 549
TYPES TANK
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APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth A.
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Best Local Similarity
Matches 17; Conserv
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 526
OTHER INFORMATION: n = A,T,C or G
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Stolk, John A.
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Indirias, Carol Yoseph
Lodes, Michael J.
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Carter, Darrick
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-135561
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PRIOR ETILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 135561
                                                              Matches
                                                                                            Query Match
                                                                                                                                                                            LENGTH: 602
                                                     B2.0%;
Local Similarity 94.4%;
les 17; Conservative
 442 TGTTGCTTAAGATTTTTT
                               3 TGTTGCTTAAGCTTTTTT 20
                                                              0; Mismatches
                                                                                Score 16.4;
Pred. No. 9
                                                                                9e+02;
                                                                                               DB 13;
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Search completed: August Job time : 9.18607 secs 1, 2003, 13:37:01

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Maximum DB seq length: 2000000000
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  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfIles1.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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4 US-09-328-352-1157
3 US-09-301-085-157
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9 US-09-643-615A-11
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Sequence 3, Appli
Sequence 3726, Ap
Sequence 1158, Ap
Sequence 1157, App
Sequence 157, App
Sequence 157, App
Sequence 157, App
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	SULT 1 -09-328-35 Sequence 2 Patent No. Patent No. PAPLICANY TITLE OF TITLE OF FILE REFI CURRENT 1 NUMBER 0. SEQ ID NO. LENGTH: TYPE. DO ORGANIS -09-328-3 Query Mat Best Loca Matches Matches	44444000000000000000000000000000000000
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3 5518 FAMAT YEMAT VENT VENT VENT VENT VENT VENT VENT VEN	ESULT 1  S-09-352-2249/c Sequence 2249, Application US/09329 Sequence 2249, Application US/09329 Sequence 2249, Application US/09329 Sequence 2249, Application US/09329 SEQUENCE OF INVENTION: NUCLEIC ACID TITLE OF INVENTION: NUCLEIC ACID TITLE OF INVENTION: BAUMANNII FOR FILE REFERENCE: GTC99-03PA CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 SEQ ID NO 2249 LENGTH: 1077 TYPE: DNA CORGANISM: Acinetobacter baumanni CORGANISM: Acinetobacter baumanni US-09-328-352-2249  Query Match Best Local Similarity 90.0%; Pr Matches 18; Conservative 0; Matches 18; Conservative 0; Matches 18; Conservative 1; Matches 18; Conservative 0; Mat	76.0 76.0 76.0 76.0 76.0 76.0 76.0 76.0
	Application US/093 62958 Application US/093 662958 AWATION: AWATION: AUCLEIC ACID JENTION: NUCLEIC ACID JENTION: BAUMANNII FO NOE: GTC99-03-PA LICATION NUMBER: US/C LICATION NU	606 606 606 606 606 606 607 1011 1011 10
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9811469 al. al. BALLER PHOSPHATASE PROTEING C ACID MOLECULES ENCODING ES THEREOF US/09/811,469 03-20 ws Version 4.0	B352  AND AMINO ACID DIAGNOSTICS AN /328,352  /328,352  i	US-09-123-912-55 US-09-643-597-55 US-09-480-884A-55 US-09-482-615A-55 US-09-522-217-108 US-09-328-552-1717 US-08-68-528A-1 US-09-456-287-1 US-08-487-429A-10 PCT-US96-05220A-119 US-09-134-01C-1995 US-09-134-01C-1995 US-09-134-01C-1995 US-09-281-16-101 US-08-487-258-4 US-09-258-784A-4 US-09-528-784A-4 US-09-528-784A-4 US-09-528-784A-4 US-09-528-784A-4 US-09-569-098A-4
HUMAN PHOSPHATASE PROTEINS,	SEQUENCES RELATING TO ACINETOBACTER ID THERAPEUTICS	Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 108, Appl Sequence 108, App Sequence 1717, Ap Sequence 1, Appli Sequence 1, Appli Sequence 10, Appl Sequence 195, App Sequence 195, App Sequence 195, App Sequence 4, Appli

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US-09-328-352-3348/c
Sequence 2348, Application US/09328352
PAtent No. 6562958
PATENT INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                        / ORGANISM: Acinetobacter baumannii
US-09-328-352-1158
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US-09-328-352-3726/c
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1158
LENGTH: 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BANDANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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Patent No. 6562958
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PATENT NO. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
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CURRENT FILING DATE: 1999-06-04
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Local Similarity 89.5%;
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100.0%; Pred. No. 1.5e+02;
Live 0; Mismatches 0; Indels (
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Pred. No. 1.7e+02;
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-2348
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Patent No. 5981730
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2348
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                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,360
FILING DATE: APT11 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mindrinos
APPLICANT: YU, Guo-L:
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30B
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MEDIUM TYPE: Floppy
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APPLICANT:
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
   / Match 79.0%; Score 15.8; DB 2; Length 5134; Local Similarity 89.5%; Pred. No. 1.8e+02; Local 17; Conservative 0; Mismatches 2; Indels 0
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                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                               TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1551
                                                                                                                                                                                                                                                                                             NAME: Lech, Karen F. REGISTRATION NUMBER:
                                                                                                                                                           LENGTH: 5134 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 79.0%;
Local Similarity 89.5%;
es 17; Conservative
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Brent, Andrew F.
Dahlbeck, Douglas
Katagiri, Fumiaki
Funiaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu, Guo-Liang
WENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08310912A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mindrinos, Michael N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ausubel, Frederick M.
                                                                                                                                                                                                                                                                                                                                                                                                                September 22, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barbara N.
                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/310,912A
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                                                                                                                                                                                                                                                                             00786/254001
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AATGTTGCTTAAGCTTTTT 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/301,085
CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER FILING DATE: 1994-09-22
EARLIER APPLICATION NUMBER: 08/227,360
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-301-085-157
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APPLICANT: Ausubel, Frederick M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 157, Application US/09301085 Patent No. 6262248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 157
LENGTH: 5134
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 157, Application PC/TUS9504589 GENERAL INFORMATION:
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APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Staskawicz, Brian J
APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Katagiri, Fumiaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
             ZIP: 02110-2904

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                    STREET:
                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                     ADDRESSEE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 AATGTTGATAAAGCTTTTT 444
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                                                                                                                                                                                  Boston
                                                                                                                                                                                                                                                                            T: Yu, Guo-Liang
INVENTION: RPS2 GENE AND USES THEREOF
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                                                                                                                                                                                                  225 Franklin Street Suite 3100
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Katagiri, Fumiaki
                                                                                                                                               USA
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     PCT/US95/04589
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Pred. No. 1.8e+02
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ATTORNEY AGENT INFORMATION:
NAME: Dow, Alan. E.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 5151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391

5151-45038

FILING DATE: September 22, 1994 CLASSIFICATION: 800

APPLICATION NUMBER:

08/310,912

FILING DATE: A CLASSIFICATION:

APPLICATION NUMBER: 08/227, FILING DATE: April 13, 1994

08/227,360

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MOLECULE TYPE:
PCT-US95-04589-157
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INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 5134 base pairs
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
Stabkawicz, Brian S., Oldroyd, Giles Edward,
APPLICANT: Stabkawicz, Brian S., Oldroyd, Giles Edward,
APPLICANT: Salmeron, John M., Rommens, Caius
APPLICANT: COMPOSITIONS AND METHODS FOR PLANT
TITLE OF INVENTION: PATHOGEN RESISTANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                               SOPTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/0
FILING DATE: July 11, 1996
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 79.0%;
Local Similarity 89.5%;
                                                                                                                                                                                                                                                                  ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Whinston STREET: One World Trade Center STREET: 121 S.W. Salmon Street
                                                                                                   MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                     CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 AATGTTGATAAAGCTTTTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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                                                                                                                                                                                                                     Oregon
                                                                                                                                                                                                                                                          Suite 1600
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                                                                                                                                                                                                  United States of America
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                                                            US/08/680,327
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Pred. No. 1.8e+02;
0; Mismatches 2; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/228,246

CURRENT FILING DATE: 1999-01-11

EARLIER APPLICATION NUMBER: 08/680,327

EARLIER FILING DATE: 1996-07-11

EARLIER APPLICATION NUMBER: 08/310,912

EARLIER FILING DATE: 1994-09-22

EARLIER APPLICATION NUMBER: 08/227,360

EARLIER APPLICATION NUMBER: 08/227,360

EARLIER APPLICATION NUMBER: 08/227,360

EARLIER FILING DATE: 1994-04-13

NUMBER OF SEQ ID NOS: 5

CORPMANDE: 03-2-7,360
                                                                                                                                                                                                                                                              Sequence 2, Application US/08680327 Patent No. 5859321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 3
; LENGTH: 5475
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-228-246-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(5475)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Staskawicz, B. S. et al.
TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: Compositions
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
                                                                                                                                      APPLICANT: Stakkwicz, Brian S., Oldroyd, Giles Edward, APPLICANT: Salmeron, John M., Rommens, Caius TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5475 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                   2508 AATGTTGATAAAGCTTTTT 2490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                        1 AATGTTGCTTAAGCTTTTT 19
                             Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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     Oregon
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Similarity 89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.8; DB 3; Length 5475; Pred. No. 1.8e+02;
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US-09-228-246-1
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US-09-228-246-1/c
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                                                                                                                                                                     SEQ ID NO
                                                                                                                                                                                                                                      FILE REFERENCE: 51700
CURRENT APPLICATION NUMBER: US/09/228,246
CURRENT FILING DATE: 1999-01-11
EARLIER APPLICATION NUMBER: 08/680,327
EARLIER FILING DATE: 1996-07-11
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER TILING DATE: 1994-09-22
EARLIER TILING DATE: 1994-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 5151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEPAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Staskawicz, B. S. et al.
TITLE OF INVENTION: PRF Protein and Nucleic Acid Sequences: (
TITLE OF INVENTION: and Methods for Plant Pathogen Resistance
FILE REFERENCE: 51700
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09228246
Patent No. 6245510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                 EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 08/227,360
       NAME/KEY: CDS
LOCATION: (8300)..(9466)
                                                                                                 TYPE: DNA
ORGANISM: Lycopersicon esculentum
FEATURE:
                                                   FEATURE:
                                                                             NAME/KEY: CDS
                                                         LOCATION: (3879)..(8186)
                                                                                                                                                   ENGTH: 10968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/227,
FILING DATE: April 13, 1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Alan. E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/6
FILING DATE: July 11, 1996
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89.5%;
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Pred. No. 1.8e+02;
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TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB193P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1 Patent No.
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/916,421B CURRENT FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: US 60/024,428 PRIOR FILING DATE: 1996-08-22
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TYPE: DNA
ORGANISM: Mycoplasma genitalium
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                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (28222)..(28)
                                                                                                                                                                         ORGANISM: Methanococcus jannaschii FEATURE:
                                                                                  NAME/KEY: misc_feature
LOCATION: (28257)..(28)
                                                                                                                    LOCATION: (28222) . (28222)
OTHER INFORMATION: n equals a,
                NAME/KEY: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
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Pred. No. 1.8e+02;
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            NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
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NAME/KEY: misc feature LOCATION: (98120)..(98120) OTHER INFORMATION: n equals LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (148948)..(148948) OTHER\_INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (103998)..(103998) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (98343)..(98343) OTHER INFORMATION: n equals LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a,
NAME/KEY: misc\_feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (234220)..(234220) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (231980)..(231980) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (191995)..(191995) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (309418)...(309418) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (234187)..(234187) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (319226)...(319226) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (312837)...(312837) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (559241)..(559241) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (559167)...(559167) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (600992)..(600992) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals NAME/KEY: misc\_feature LOCATION: (312993)..(312993) . (191989) a þ a, a, þ , Ç ŗ Ĺ , ŗ ָרָד Ĺ ŗ ŗ ζ, Ģ ņ ņ c, or g o, ú ņ Ç Ç 'n ņ ņ ç ú 'n c, or g ņ ū ó ú ņ 9 or P or g မ္ပ မ္ပ or g or g or g ç မ္ပ g ro g g õ 유 or g ę 유 ç õ 유 or g ω ω g

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NAME/KEY: misc feature LOCATION: (1470091). (1470091) OTHER INFORMATION: n equals a, t NAME/KEY: misc feature LOCATION: (1569020). (1569020) OTHER INFORMATION: n equals a, t
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NAME/KEY: misc_feature
LOCATION: (1349473)...(1349473)
OTHER INFORMATION: n equals a, t, c
NAME/KEY: misc_feature
LOCATION: (1349491)
OTHER INFORMATION: n equals a, t, c
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LOCATION: (1310988)...(1310988)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (1313224)...(1313224)
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
                                                                                 NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a,
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LOCATION: (1664854)..(1664855)
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OTHER INFORMATION: n equals a, t,
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LOCATION: (1119881)..(1119881)
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LOCATION: (1096846)..(1096846)
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LOCATION: (871619)..(871619)
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LOCATION: (1084830)..(1084830)
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LOCATION: (713652)..(713652)
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LOCATION: (657203)...(657203)
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Search completed: August 1, 2003, 08:37:17 Job time: 5.65066 secs
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                                                                                                                                      Best
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                           TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1038, App
Patent No. 6500938
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                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
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                                                                                                                                                                                                                                                                                                                                                                             NAME: Zeller, Karen J
REGISTRATION NUMBER:
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Local Similarity 89.5%;
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                         77.0%; Score 15.4; DB 4; 94.1%; Pred. No. 2.6e+02;
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Pred. No. 1.4e+02;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a
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10468.541 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|            | 45           | 43                                                            | 42                                                                                                                                        | 4.                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                   | ມຜ                                                                                                                                                                                                                                | c<br>37                                                                     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Eukaryota; Metazoa; Chordata; Craniata; verteurata; butteria; Primates; Catarrhini; Hominidae; Homo.	ni; Homini	Catarrhi	mates;	etazoa; Cho theria; Pri	Eukaryota; Metazoa; Chordata; Craniaca; vertebraca; buccac Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
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Brandi, M.
Direct Submission
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Rattus norvegicus (Norway rat)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                   Bianchi,S., Fabiani,S., Muratori,M., Arnold,A., Sakaguchi,K.,
Miki,T. and Brandi,M.L.
Calcium modulates the cyclin D1 expression in a rat parathyroid
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                                                             Biochem. Biophys. Res. Commun. 204 (2), 691-700
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Novak, J.E., Presnell, S.R., Sprecher, C.A., Foster, D.C., I Gross, J.A., Johnston, J.V., Nelson, A.J., Dillon, S.R. and Hammond, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine zalphall Ligand Patent: US 6307024-A 108 23-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: k Column: 9
                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                          Center code: BCM-HGSC
                                                                                                                                                                                                                                                Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC044841.1 GI:27924088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC044841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 2358)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358
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/db_xref="GI:473123"
/db_xxef="SWISS_PROT:P39948"
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Pred. No. 2.4e+03;
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                                                                                                                                                                                                                                                                                                                                Chu-Xia Deng
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ORIGIN
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Best Local (
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Local Similarity 95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to protein
 1440 AATGTTTCTTAAGCTTTTTT 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                       AX695351.1 GI:29418501
                                                                                                                                                                                                                                           Sagres Discovery (US)
                                                                                                                                                                                                                                                         Novel compositions and methods for cancer patent: WO 03008583-A 978 30-UAN-2003;
                                                                                                                                                                                                                                                                                          Morris, D.W. and Engelhard, E.K.
                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                    1 AATGITTCTTAAGATTTTTT 20
|||||||||||||||
                                                                                 Similarity
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                                                                   Conservative
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/translation="MEHOLLCCEVETIRRAYPDINILINDRVLRAMLKTEETCAPSVSY
/translation="MEHOLLCCEVETIRRAYPDINILINDRVLRAMLKTEETCAPSVSY
/translation="MEHOLLCCEVETIRRAYPDINILINDRVLRAMLKTEETCAPEX
FKCYQKEIVPSMRKIVATMMLEVCEEQKCEEVFFLANNYLLFRLAMTPHDF
GATCMFVASKMKETIPLTAEKLCIYTNNSIRPEELLQMELLLVNKLKMULLAAMTPHDF
GATCMFVASKMKETIPLTAKHAQTFVALCATDVKFISNPPSMVAAGSVVAAMQGLNLG
IEHFLSKMFEADENKQTIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAAMQGLNLG
SPNNFLSCYKTTHFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQNVDPKATEEEGE
SPNNFLSCYKTTHFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQNVDPKATEEEGE
SPNNFLSCYKTTHFLSRVIKCDPDCLRACQEQIEALLESSLRQAQQNVDPKATEEEGE
VEEEAGLACTPTDVRDVDI"

8 587 c 617 g 543 t
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/clone lib="NCI_CGAP_Mam3"
/lab_host="DH10B"
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/strain="129,C57BL/6J,FVB/N"
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/clone="MGC:7003 IMAGE:3155470"
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/protein id="AAH44841.1"
/db_xref="GI:27924089"
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                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                   /mol_type="genomic DNA
/db_xref="taxon:10090"
/004 c 988 g
                                                                                                                                                                                                                             Location/Qualifiers
                                                                                    92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.4; DB 10;
Pred. No. 2.1e+03;
                                                                        0; Mismatches
                                                                                      Score 18.4;
Pred. No. 1.
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                                                                                        1.9e+03;
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                                                                                                         DB 6; Length 3737;
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S78355/c
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ACCESSION
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VERSION
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1440 AATGTTTCTTAAGCTTTTT 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyl-1=cyclin D1 [mice, BALB/c, brain, mRNA, 3737 nt].
S78355
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Rattus rattus mRNA for cyclin D1, complete cds.
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus (black rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D14014.1 GI:413908
Oncogene 8 (8), 2113-2118 (1993)
93330551
                                                                                                                      Tamura,K., Kanaoka,Y., Jinno,S., Nagata,A., Ogiso,Y., Shimizu,K., Hayakawa,T., Nojima,H. and Okayama,H. Cyclin G: a new mammalian cyclin with homology to fission yeast
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                                                                                                                             Submitted (16-APR-1998) Zoology,
                                                                                                                                                                                                                 Microsporidia are related to Fungi: evidence from the largest subunit of RNA polymerase II and other proteins Proc. Natl. Acad. Sci. U.S.A. 96 (2), 580-585 (1999)
                                                                                                                                                     Direct Submission
                                                                                                                                                                       Hirt, R.P.
                                                                                                                                                                                                                                                                 Eukaryota, Fungi; Microsporidia; Burenellidae; Vairimorpha.

1 (bases 1 to 5019)

Hirt, R. P., Logsdon, J. M. Jr., Healy, B., Dorey, M.W., Doolittle, W.F. and Embley, T.M.
                                                                                                                                                                                                                                                                                                                                              Vairimorpha necatrix
                                                                                                                                                                                                          9892676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-JAN 1993) Yuko Ogiso, Research Development Corporation of Japan, Okayama Cell Switching Project; Pasteur Building 4F,103-5 Tanaka Monzen-cho, Bakyo-ku, Kyoto, Kyoto 606 Japan (Tel:81-75-712-5406, Fax:81-75-712-5492)
                                                                                                                                                                                     (bases 1 to 5019)
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                      /mol_type="genomic by
/db_xref="taxon:6039
101: .4918
                                                           organism="Vairimorpha necatrix"
                                                                                               Location/Qualifiers
     gene≈"RPB1"
                                                                                                                                                                and Healy, B.
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PKCVQREIVPSWRKIVATWMLBVCEEQKCEEEVFPLAMNYLDRFLSLEPLKKSRLQLL

GATCMFVASKMKETIPLTAEKLCIYTNSIRPEELLQMELLLVNKLKWNLAAMTPHDF

IEHFLSKWPEADENKQIIRKHAQTFVALCATDVKFISNPPSMVAAGSVVAAMQGLNLG

VEPEAGLACTPTDVRDVDI"
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/protein_id="BAA03115.1"
/db_xref="GI:413909"
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/clone_lib="pcD2 NRK cDNA library"
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                                                                                                                London SW7 5BD,
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l_line="NRK-49F"
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                                                                                                                     Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10212590 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neoptera; Endopterygota; Diptera; Brach
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 5226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC014915 5226 bp DNA linear HTG 16-NOV-1999 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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D.melanogaster genes for histone H3.3 and OST48.
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prosophila melanogaster (fruit fly)
prosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Submitted (03-SEP-1994) A.S. Akhmanova, Catholic University of
Submitted (03-SEP-1994) A.S. Akhmanova, Catholic University of
Nijmegen, Dept of Molecular & Developmental, Genetics,
Toernooiveld, 6525 ED Nijmegen, NETHERLANDS
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/codon_start=1
/product="0.11gosaccharyltransferase 48kDa subunit"
/product="0.11gosaccharyltransferase 48kDa subunit"
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/product="0.11gosaccharyltransferase 48kDa subunit"
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/db_xref="F0.12963028"
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/mol type="genomic DNA"
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      3304. .3609
                                                              /gene="histone H3.3"
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Local Similarity 95.0%;
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                                                                                                                                                                                                                                                                                                       synthetic construct
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Diagnosis of diseases associated with the immune system
Patent: WO 020928-A 12 03-UAN-2002;
                                                                                                                                                                                                                                                                                              synthetic construct
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    1 AATGTTTCTTAAGATTTTTT 20
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GTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSAAIGALQEASEAYLV
GLFEDTMULCAIHAKRVTIMPKDIQLARRIRGERA"
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/db_xref="taxon:32630"
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/note="chemically treated genomic DNA (Homo sapiens)"
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                                                          1 AATGTTTCTTAAGATTTTTT 20
                                                                                                                                                                                                                                                                                             Sagres Discovery (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              Novel compositions and methods for cancer Patent: WO 03008583-A 977 30-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                  Morris, D.W. and Engelhard, E.K.
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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This sequence was identified as CDM:10210291 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * by the finished sequence as soon as it is available and * the accession number will be preserved.
                                                                                                                                                                                                           6341 a
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Reoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
CEK10H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                         Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL,
                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBMED
                                                                                                                                                                                                                                                                          IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15914 AATGTTTCTTAAGCTTTTTT 15895
                                                                                                                                                                                                                                                                                                                                                                                       For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 283110.

The true left end of clone F57C2 is at 29930 in this sequence. The true right end of clone C13B4 is at 19748 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               The end of this sequence (29930. .30033) overlaps with the start of sequence Z83110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a grammatic reaction, from distinct subclones. It may be shorter because we only sequence once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neighbouring submissions.
The true left end of clone K10H10 is at 1 in this sequence. The
true right end of clone K10H10 is at 7962 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-DEC-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CBIO 1SA, England and Department of Genetics, Mashington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The C.elegans Sequencing Consortium 2 (bases 1 to 30033)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percy, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium concert, 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans cosmid K10H10, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z83236.1 GI:1729646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEK10H10
/gene="usp-14"
join(complement(1..212),complement(Z81468.1:23725..24037),
complement(Z81468.1:22690..23349),
complement(Z81468.1:21450..21734))
                                                                               join(Complement(1. .212), complement(Z81468.1:23725. .24037), complement(Z81468.1:23690. .23349), complement(Z81468.1:21450. .21734))
                                                                                                                                                                                                         /organism="Caenorhabditis elegans"
/mol_type="genomic_DNA"
/strain="Bristol_N2"
                                                                                                                                                           /clone="K10H10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
                                                                                                                                                                                chromosome="II"
                                                                                                                                                                                              _xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30033 bp
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/note="contains similarity to Pfam domain: PP00442 (Ubiquitin carboxyl-terminal hydrolases family 2), Score=31.3, E-value=3.1e-06, N=1; PP00443 (Ubiquitin carboxyl-terminal hydrolase family 2), Score=108.6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yk143a12.5 comes from this gene
cDNA EST yk173f1.5 comes from this gene; cDNA EST
yk187b6.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yk119a8.5 comes from this gene cDNA EST cDNA EST yk143a12.3 comes from this gene; cDNA EST yk173f1.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA EST yk455e2.5 comes from this gene; cDNA EST yk191g6.3 comes from this gene cDNA EST yk269a1.3 comes from this gene; cDNA EST yk269a1.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA EST yk187b6.3 comes from this gene; cDNA EST yk143a12.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-value=4e-29, N=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yk619d1.5 comes from this gene CDNA EST cDNA EST yk623a10.5 comes from this gene; cDNA EST yk770e04.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA EST yk269a1.5 comes from this gene; cDNA EST yk282f4.5 comes from this gene cDNA EST yk282f6.5 comes from this gene; cDNA EST yk364h11.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA EST yk391b5.3 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA EST yk283f6.3 comes from this gene; cDNA EST yk264h11.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA EST yk190b4.5 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA EST yk119a8.3 comes from this gene; cDNA EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="usp-l4"
/standard_name="Cl3B4.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yk1061a11.3 comes from this gene, cDNA EST cDNA EST yk1188b05.5 comes from this gene; cDNA EST yk1188b05.3 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yk832e05.5 comes from this gene cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yk619d1.3 comes from this gene
cDNA EST yk623a10.3 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA EST yk391b5.5 comes from this gene; cDNA EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                IMGRTLGDDDWEGITIKENMTIMMGSVGEIPKPPTVLEKKQANRDKQAEEISALYPC
GLANLGNTCYFNSCVQMLKEVNELVLKPAEEMRIREHNDRLCHNLATLFNSLRDKDRA
LRSKGEPIKPFAAILTLSDSFPQFEKFKQQDANECLVSIMSNVTRIYGLSGWNIESLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA EST yk1290c12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA EST U32223 comes from this gene; cDNA EST yk1278e05.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence C13B4.2) "
/protein_id="CAB05785.1"
/db_xref="GI:3878545"
                                                                                                                                                                                               2359. .2561,3265. .3739,3923. .4095)
/gene="K10H10.1"
                                                                                                                                                                                                                                                             YVLLYEARVIKQFPELPPAPVPTEVAADTAEPMEVSEKQ"
join(1338. .1390,1450. .1576,1641. .1727
                                                                                                                                                                                                                                                                                                                                                                                         RIQTETTMKCLESDEVSEKKVERNNQLTCYVNQDVRFLQTGIKAGFEEEMTRNSEELN
RDAKWQKNTQISRLPKYLTVNINRFFYKESTKTNAKILKSVQFPMQLDTYDLCSQELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         k1290c12.3 comes from this gene"
                                                                                                        2359. .2561,3265. .3739,3923. .4095)
/gene="K10H10.1"
                                                                                                                                                                                                                                                                                                                           DLKGIITHKGRSSQDGHYVAWMRSSEDGKWRLFDDEHVTVVDEEAILKTSGGGDWHSA
                                                                                                                                                                                                                                                                                                                                                            DKLVARRAD I KLEEDAKLERELRKKVLDKEQGDK I FDDGVAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GOA:Q17361"
/db_xref="SWISS-PROT:Q17361"
/translation="MPIVNVKWQKEKYVVEVDTSAPPMVFKAQLFALTQVVPERQKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="C. elegans USP-14 protein (corresponding
                                             note="contains similarity to Pfam domain: PF00083 (Sugar
                                                                                                                                                                  oin(1338. .1390,1450. .1576,1641. .1727,1778. .1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
             (and other) transporter), Score=-89.7, E-value=0.00037
                                                                       standard_name="K10H10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST yk832e05.3 comes from this gene; cDNA EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                    .1727,1778.
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LOCUS
                          CEK04H4/c
                                                          RESULT 15
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                     14322
                                                                                                                                                                                                                                                                          19;
CEK04H4
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gene

33930 bp

DNA

linear

INV 21-MAY-2003

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1 AATGTTTCTTAAGATTTTT 20
                                                                                                                                                      Similarity
AATGTTTCTTAAAATTTTTT 14341
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                           CDNA EST yk31393.5 comes from this gene; cDNA EST yk393g6.5 comes from this gene cDNA EST yk419f11.5 comes from this gene; cDNA EST yk425c10.5 comes from this gene; cDNA EST yk425c10.5 comes from this gene; cDNA EST yk461h2.5 comes from this gene; cDNA EST yk461h2.5 comes from this gene; cDNA EST yk481h2.5 comes from this gene; cDNA EST yk483d3.5 comes from this gene; cDNA EST yk483d3.5 comes from this gene; cDNA EST yk483d3.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLGIAFCLMLVPMTSSFWISLIIFTMAMAARGLHHGGVSVNPHDFAPNHAGSVFGVFN
ACGAITGFVGVYIAGHILEATNNNWSYVFVVTAAQCVVGAMVYTLLGTGQKII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA EST yk425c10.3 comes from this gene; cDNA EST yk432b7.3 comes from this gene cDNA EST yk450f7.3 comes from this gene; cDNA EST yk461h2.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA EST yk186f5.3 comes from this gene; cDNA EST yk186a12.5 comes from this gene cDNA EST yk184173c5.5 comes from this gene; cDNA EST yk186f5.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join(4481. .4583,4938. .5172,5274. .5949))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (join (4481. .4583, 4938. .5172, 5274. .5949)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFTPHLFDFAYWTNYPLVVLLAVRILTGVCQAFHIPSLASIVSKHLAAADKGRVFGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAAAVAKEFAWNKTDSGTVLSCFFWGYALTQVFAGRIADKYGAEKILPYSSLAWTMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yk334g3.3 comes from this gene cDNA EST cDNA EST yk393g6.3 comes from this gene; cDNA EST yk418f11.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA EST yk156a12.3 comes from this gene; cDNA EST yk173c5.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA EST yk115e1.5 comes from this gene; cDNA EST yk115e1.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLPSYFHETFPTAKGFVYNVVPSLAIVVTSLVAPVMASRALSEGKTVTYTRKLMEGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPDEEVLLDKKHDTIESHLAATSPCPSVPWGTLFRHPAFWAAAVAQYTGGNSYSILFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGSHWGTVLAGAIGSILIEWIGWRALFQFVGIISLIWCWVFRWVLDRAKGPGGRSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA EST yk483d3.3 comes from this gene; cDNA EST yk290d2.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA EST yk481e10.3 comes from this gene; cDNA EST yk410h8.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA EST yk466c5.3 comes from this gene; cDNA EST yk481e1.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA EST yk290d2.3 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-value=2.6e-125,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="contains similarity to Pfam domain: PF00291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="K10H10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:045678"
/translation="MLKRPGEYEPPLGKIWTRAESRMWTITMFSGTCVLYASRASLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Pyridoxal-phosphate dependent enzyme), Score=428.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="K10H10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard_name="K10H10.2"
                                                                                                                                                                                                                                                    cDNA EST yk519h5.3 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xref="GOA:045678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xref="GI:3878537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST yk503h12.5 comes from this gene EST yk653all.3 comes from this gene EST yk653all.5 comes from this gene"
                                                                                                                                                         92.0%;
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                                                                                                                        Score 18.4; DB 3; Length 30033; pred. No. 1.1e+03; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N=1
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7.1"
                                                                                                                                         Gaps
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DEFINITION

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FEATURES
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                        SdC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlapping sections once, or longer because we arrange for overlap between neighbouring submissions. [020311 dl] T->G at position 3143 based on Thierry-Mieg EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence Z19154. The end of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone K04H4. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-NOV-1993) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: Jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 14, 2002 this sequence version replaced gi:19571633.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neighbouring submissions.
The start of this sequence (1. .97) overlaps with the end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [021031 ar2] + G at 6588 position based on EST alignment [021031 ar2] -C at position 6808 based on EST alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the specified clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    name=K04H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence Z19153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [020311 dl] - T at position 4618 based on Thierry-Mieg EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [020311 dl] + C at position 4614 based on Thierry-Mieg EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          available information.

Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans cosmid K04H4, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99069613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z27078.3 GI:25004984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end of this sequence (33837. .33930) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.elegans Sequencing Consortium (bases 1 to 33930)
                                                                                                                                                                                                                    complement(join(1214. .1309,1727. .2508,2567. .3839, 3929. .4789,4844. .5086,5180. .5434,5491. .6515,6573. .6975, 7381. .7532,7941. .8107,8382. .8449))
                                                                                               complement(join(1214. .1309,1727. .2508,2567. .3839, 3929. .4789,4844. .5086,5180. .5434,5491. .6515,6573. .6975, 7381. .7332,7941. .8107,8382. .8449))
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans"
/mol_type="genomic DNA"
/strain="Bristol N2"
note="similar to collagens, contains similarity to Pfam
                                                                                                                                                                                                                                                                                                                   /clone="K04H4"
                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:6239"
/chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                         standard_name="K04H4.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is NOT necessarily the entire insert of ied clone. It may be shorter because we only sequence g sections once, or longer because we arrange for a small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .33930
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/translation="msrlsllgltaavVllssfcQDr1HVDaaaackgcappcVcPgTKgERGNPGFGEEPGHPGAPGADGDEGAPGAPGAPGAEGDFGDMGSKGARGDRGLPGSPGHPGLAGGDGEEPGHPGAPGAPGAPGAPGAEGDFGDMGSKGARGDRGLPGSPGGHPGLAGLDGLPGLKGEEGIPGCNGTDGFPGMPGLAGPPGQSGQNGNPGRPGLSGPPGGHPGGEGGRPGGEGGRMSQGRMSQGRKGVKGESGRSGVPGLPGNSGYPGLKGAKGDPGPYGLPGFPGVSGLKGRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yk1313a04.3 comes from this gene yk1025a11.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yk1202a01.3 comes from this gene
CDNA EST yk1278a06.5 comes from this gene; cDNA EST
yk1278a06.3 comes from this gene
CDNA EST yk1285a06.5 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="C. elegans EMB-9
KO4H4.1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA EST yk1313a04.5 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA EST yk1068f08.5 comes from this gene; cDNA EST yk1068f08.3 comes from this gene cDNA EST yk1113c11.3 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yk878c05.5 comes from this gene cDNA EST yk102sf07.3 comes from this gene; cDNA EST yk102sc02.5 comes from this gene cDNA EST yk1053c02.3 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA81584.3"
/db_xref="GI:25004987"
/db_xref="GOA:P17139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yk1285d05.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA EST yk1285d05.5 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yk1062a05.5 comes from this gene cDNA EST yk1062a05.3 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yk776h06.5 comes from this gene cDNA EST yk878c05.3 comes from this gene; cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yk501e3.5 comes from this gene
cDNA EST yk755c11.3 comes from this gene; cDNA EST
yk755c11.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA EST yk374e1.5 comes from this gene; CDNA EST yk425h10.5 comes from this gene CDNA EST yk654a8.3 comes from this gene; CDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yk1285a06.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yk1068c10.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA EST yk776h06.3 comes from this gene; cDNA EST yk776h06.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yk425h10.3 comes from this gene cDNA EST yk501e3.3 comes from this gene; cDNA EST yk204d3.5 comes from this gene; cDNA EST yk204d3.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=689.9, E-value=4e-204, N=21; PF01413 (C-terminal tandem repeated domain in type 4 procollagen), Score=500.5, E-value=4e-147, N=2 cDNA EST CEESO09F comes from this gene; cDNA EST yk108f8.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="SWISS-PROT:P17139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comes from this gene
cDNA EST yk108f8.3 comes from this gene; cDNA EST
yk284d3.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA EST yk95b4.5 comes from this gene; cDNA EST yk95b4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comes from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein (corresponding sequence
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EAGEPGTPGYRGQPGEPGNLAYPGQPGDVGYPGDDGPPGLPGLPGLNGERGDNGD QPGLEGECGEDGFPGSPGQPGYPGQQGREGEKGYPGIPGENGLPGLRGQDGQPGLKGE

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Search completed: August 1, 2003, 17:33:02 Job time : 81.1573 secs
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                           1 AATGTTTCTTAAGATTTTTT 20
||||||||||||||||||||||||
27620 AATGTTTCTAAAGATTTTTT 27601
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DTSVPQCPQGWSGMWTGYSFVWHTAAGAEGTGQSLQSPGSCLEEFRAVFFIECHGRGT

CNYYATNHGFWLSIVDQDKQFRKPMSQTLKAGGLKDRVSRCQVCLKNR"

COMPLEMENT (join(12237. 12310,11321. 13424,13503. 14186,

14233. 14349,14404. 14532,14581. 114640,15291. 15416,

17577. 17674,17719. 17821,18713. 18852,18900. 19017,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGLDGQPGYPGSAGQLGTPGDVGYPGAPGENGDNGNQGRDGQPGLRGESGQPGQPGLP
GRDGQPGPVGPPGDDGYPGAPGQDIYGPPGQAGQDGYPGLDGLPGAPGLNGEEGSPGQ
YGMPGLPGGPGESGLPGYPGERGLPGLDGKRGHDGLPGAPGVPGLEGDCGED
GYPGAPGAPGSNGYPGERGLPGVPGQQGRSGDNGYPGAPGQPGIKGPRGDDGFPGRDG
LDGLPGRPGREGLPGYPGQQGPGENGYPGEKGYPGLPGDNGLSGPPGKAGYP
GAPGTDGYPGPPGLSGMPGHGGDQGPQGAAGRTGNPGLPGTPGYPGSPGGWAPSRGFT
FAKHSQTTTAVPQCPPGASQLWEGYSLLYVQGNGRASGQDLGQPGSCLSKFNTWPFMFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join(12237. .12310,13221. .13424,13503. .14186, 14233. .14349,14404. .14532,14581. .14640,15591. .15416, 17577. .17674,17719. .17821,18713. .18852,18900. .19017, 19362. .19395))
//gene="K04H4.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(12237. .12310,12534. .12674,13221. .13424, 13503. .14186,14233. .14349,14404. .14532,14581. .14640, 15291. .15416,17577. .17674,17719. .17821,18713. .18852, 18900. .19017,19362. .19395))
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CDNA
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/note="similar to Chitin-binding motifs
cDNA EST yk133d11.5 comes from this gen
                                                                                                                                                                                                                                                                                                                                                                        NA EST yk43493.5 comes from this gene
NA EST yk13d11.3 comes from this gene
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Listing first 45 summaries
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TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AV243724/c LOCUS DEFINITION		C 43 11 C 44 11 45 11
			S AV243724 EST 04-NOV-1999  AV243724 RIKEN full-length enriched, 0 day neonate head Mus N AV243724 RIKEN full-length enriched, 0 day neonate head Mus musculus cDNA clone 4831423J17 3' similar to S78355 Cyl-1=cyclin D1	ALIGNMENTS	18.4 92.0 570 14 CA873049 18.4 92.0 572 28 BZ175552 18.4 92.0 572 29 BZ611328  18.4 92.0 572 29 BZ611328  BZ611328 WHAAN04TF

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AV174680/c
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         5730411L18, mRNA sequence.
AV174680
AV174680.1 GI:5381118
                                                               AV174680 Mus musculus C57BL/6J 8-day embryo Mus musculus CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contributed to prepare mouse tissues. 1st strand cDNA was
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 AATGTTTCTTAAGCTTTTTT 136
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
                                                                                                        Other_ESTs: uo44d03.y1
                                                                                                                                 Unpublished
                                                                                                                                                          Tumor Gene Index
                                                                                                                                                             NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 198)
                                                                                                                                                                                                                                                                                                                                                                                                                             AW213875 198 bp mRNA linear EST 03-DEC-199 u044403.x1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:2645381 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AATGTTTCTTAAGATTTTTT 20
                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
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1 (bases 1 to 160)

Carrinci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
A. Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara
A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara
Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
RIKEN Mouse ESTs

RIKEN Mouse ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone_lib="Mus musculus C57BL/6J 8-day embryo"
27 c 34 g 57 t 2 others
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
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Pred. No. 1.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels 0;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
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                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Kikuchi, N., Kojima, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
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AVI34425 Mus musculus C57BL/6J 10-11 day embryo Mus musculus CDNA clone 2810006L11, mRNA sequence.
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AV134425.1 GI:5320155
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                   Thermostabilization and thermostabration of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                         3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Mouse ESTs
                                                                                                                                                                                                                                                                                               RIKEN
                                                                                                                                                                                                                                                                                                                         Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                   Contact:
                                                                                                                                                                                Email: genome-res@rtc.riken.go.jp
                                                                                                                                                                                                          Fax: 81-298-36-9098
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further details.
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Oligo dT.
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
a 38 c 23 g 81 t
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                                                                                                                                                                                                                                                                                                                                                      Chie Owa
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Uyg-MC(B) cDNA Mus musculus cDNA clone G930031G12 3', mRNA
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                                                                                                                                                                                                                                                                                                                     Email: genome-res@gcc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carrinci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
(Carrinci.P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
prepare full-length cDNA libraries for rapid discovery of new
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-7-22 Suehiro-cho,
                                                                                                                                                                                               sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                         Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system -- 384-format
                                                                                                                                                            Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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/clone="2810006L11"
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95.0%;
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Pred. No. 1.
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nittsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                     Thermostabilization and thermostavation of thermolabile enzymes k trehalose and its application for the synthesis of full length cDN (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@rtc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Mouse ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV133072 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA
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AV133072
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Similarity 95.0%;
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                83 a
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/dev_stage="11-day embryo"
/clone_lib="Mus musculus C57BL/6J 11-day embryo"
27 c 49 g 78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chie Owa
                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
                                                                                             /clone="2700095E14"
                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                              ocation/Qualifiers
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/cell_line="RCB-0527 Jyg-MC(B)"
/clone_lib="RIKEN full-length enriched, mammary gland
RCB-0527 Jyg-MC(B) cDNA"
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Pred. No. 1.5e+04;
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Local Similarity 95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                             ,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P. Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishik, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Kadawa, H., Kadota, K., Kagawa, I., Kal, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toyasuki, H., Yaunishi, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, RIKEN Mouse ESTS (Konno, H., et al.)
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                                                                                                                                                                                                                                                                                                     further details
                                                                                                                                                                                                                                                                                                                                                          19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB048825 240 bp mRNA linear EST 25-JUN-2000 BB048825 RIKEN full-length enriched, adult male olfactory bulb Mus musculus cDNA clone 6430596J05 3' similar to S78355 Cyl-l=cyclin D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AATGTTTCTTAAGATTTTTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB048825.1 GI:8455973
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                                                                                                                                                                                                                                                                                                        visit our web site (http://genome.rtc.riken.go.jp) for
                                                        /sex="male"
                     tissue_type="olfactory brain"
                                                                                    clone="6430596J05"
                                                                                                                                            /strain="C57BL/6J"
                                                                                                                                                                                 )
mol
                                                                                                                                                                                                    organism="Mus musculus")
                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                         . 240
_stage="adult"
                                                                                                                                                                              mRNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.

25 1 (bases 1 to 255)

RS (Conno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
RS (Konno, H., Aizawa, K., Akahira, S., Fukunishi, Y., Hara, A., Hayatsu, M.,
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, M.,
P, Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, M.,
P, Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, M.,
P, Endo, T., Fukuda, S., Fukunishi, S., Kurihara, C., Kusakabe, M.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Kiyosawa, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, K., Shibata,
Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y.,
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Tominaga, N., Toya,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya,
T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino,
M., Muramatsu, M. and Hayashizaki, Y.,
PIKRN Monsa RSTE (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AATGITTCTTAAGCITTTT 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB546588 RIKEN full-length enriched, 0 day neonate eyeball Mus musculus cDNA clone E130310020 3' similar to S78355 Cyl-1-cyclin D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB546588.1 GI:9618016
Email: genome-res@gsc.riken.go.jp,
uRL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute, The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Mouse ESTs (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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                                                                                                                                                                                               81-45-503-9216
                                                                                                                                                                                                                               81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male olfactory bulb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 10.0. Second to Rot = 10.0 and subtraction to Rot = 10.0. Second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primed with a primer [5' GAGAGAGAGAGAGAGACCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.0%;
95.0%;
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Pred. No. 1.5e+04; |
0; Mismatches 1; Indels 0
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BASE COUNT

BB546588/c

RESULT

DEFINITION

REFERENCE

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 AATGITTCTTAAGCTTTTT 229
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Carninci,P and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-44 (1999)
               Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara A., Hayatsu, N., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Mutamatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                    AV135706 AV135706 Mus musculus C57BL/6J 10-11 day embryo Mus musculus CDNA
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                                                                                                                                                                                                                                                                                                                      EST.
                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 270)
                                                                                                                                                                                                                                                                                                                                                                AV135706
                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                clone 2810020K08, mRNA sequence
                                                                                                                                                                                                                                                                                                                                          AV135706.1 GI:5321436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        visit our web site (http://genome.rtc.riken.go.jp) for
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/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18.4; DB 10;
Pred. No. 1.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 255;
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 AATGITTCTTAAGCTTTTT 246
                                                                                                                                    Email: bento-soares@uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                                                    POLYA=No.
                                                                                                        Seq primer: M13 Forward
                                                                                                                        Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                   Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                               University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242,
                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI289904 278 bp mRNA linear EST 19-JUL-
UI-R-DKO-cfp-f-04-0-UI s1 UI-R-DKO Rattus norvegicus cDNA clone
UI-R-DKO-cfp-f-04-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                       8889548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery
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Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI289904.1 GI:14947954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998)) Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@rtc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
/organism="Rattus norvegicus"
/mol_type="mRNA"
                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="10-11 day embryo"
/clone_lib="Mus musculus C57BL/6J 10-11 day embryo"
34 c 61 g 87 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="2810020K08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%;
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Pred. No. 1.5e+04;
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Query Match
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 280)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Firozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB049315
280 bp mRNA linear EST 25-JUN-2000
BB049315 RIKEN full-length enriched, adult male cerebellum Mus
musculus cDNA clone 6530404H10 3' similar to 878355 Cyl-1=cyclin D1
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library, plasmid DNA from each of the five individually tagged normalized libraries was mixed in the proportions specified above and electroporated into competent bacteria for production of single-stranded circular DNA representing the pool of libraries. Single-stranded circular DNA representing these five normalized libraries was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (CTOs), heart (CSOs), kidney (CUOs), and placenta (CXOs). The resulting pool of approximately 5,000 clones represented about 3,3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CTO), heart (CSO), kidney (CUO), aorta (CWO), and placenta (CXO). The resulting pool of placenta (CXO). The resulting pool of brain placenta (CXO). The resulting pool of about 10,000 clones represented about 6.6% of the final driver population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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/clone lib="Ul-R-DKO"
/note="Wector: pT773D-Pac (Pharmacia) with a modified
/note="Wector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The Ul-R-DKO
library is a subtracted library-derived from a mixture of
five individually tagged normalized rat libraries:
brain-nRBP (20%), heart-nRHP (20%), kidney-nRKP (20%),
aorta-nRAP (20%), and placenta-nRPP (20%). Each original
library was constructed from a mixture of equal amounts of
RNA from seven different developmental time-points:
embryonic day 17, embryonic day 19, embryonic day 21,
adult day 1, adult day 12, adult day 75, and adult day
200. (Exception: the aorta pool does not contain embryonic
day 17 RNA and the placenta pool contains only the three
embryonic stages). Each library was normalized
individually according to the procedure described by
Bonaldo, Lennon & Soares (Genome Research Genome 6:
791-806, 1996). For construction of the DKO subtracted
library. nlasmid nNA from each of the EKO Subtracted
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/db_xref="taxon:10116"
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95.0%;
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Pred. No. 1.5e+04;
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REFERENCE

KEYWORDS VERSION ACCESSION

ORGANISM

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Matches

Local

BASE COUNT

BB049315/c LOCUS

RESULT 11

DEFINITION

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COMMENT
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URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Carninoi,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
Carninoi,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
N., Okazaki,Y., Muramatsu,M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of the Toth I length
trehalose and its application for the synthesis of full length
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Toh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Okazaki
Tomaru,Y., Carrinci, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,M., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Konno,H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, F. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-45-503-9222
  266 AATGTTTCTTAAGCTTTTT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                          1 AATGITTCTTAAGATTTTTT 20
                                                                                                                                         Similarity
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                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in GRIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                   3']. cDNA was cloned into the KhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                           92.0%;
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DEFINITION
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                                                  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

Clone distribution: NCI-CGAP clone distribution information can be
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF323470.1 GI:11273070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
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                                                                                                                                                                                AV219191 RIKEN full-length enriched, 12 days embryo head Mus musculus cDNA clone 3010086E05 3' similar to S78355 Cyl-1=cyclin D1 (mice, BALB/c, brain, mRNA, 3737 nt), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AATGTTTCTTAAGATTTTTT 20
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                           Mus musculus (house mouse)
                                                                                                                                      AV219191.1 GI:6168368
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/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Sall;
/note="Organ: lung; Vector: prowner; Oligo dT.
Site 2: NotI; Cloned unidirectionally. Primer; Oligo dT.
Site 2: NotI; Cloned unidirectionally. Primer; Oligo dT.
Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

57 c 40 g 99 t
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/lab_host="DH10B"
/lab_host="DH10B"
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/strain="CZECH II"
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pred. No. 1.5e+04;
0; Mismatches 1;
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REFERENCE AUTHORS

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,

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BASE COUNT
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                                                                                                                                       Local
293 AATGTTTCTTAAGCTTTTTT 274
                                 1 AATGTTTCTTAAGATTTTTT 20
                                                                                                           19;
                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Yonaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y., Akiyama,Y., Ozawa,Y., Muramatsu,M., Okazaki, Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Yoshiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
                                                                                                        Conservative
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                                                                                                                                                                                                   /note="Site 1: XhOI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                     contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      head"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="12 days embryo"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="3010086E05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
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                                                                                                                     92.0%;
95.0%;
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                                                                                                                        Score 18.4; DB 9; Length 298; Pred. No. 1.5e+04;
                                                                                              Mismatches
                                                                                                                  1.5e+04;
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ACCESSION
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                                                                            ORGANISM
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AV032131/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     Homo sapiens
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AQ072724

HS_2255_A1_D10 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=19 Row=6, genomic survey
                                                                                        Homo sapiens (human)
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                                                                                                                                        AQ072724.1
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Thermostabilization and thermoattivation of thermolabile enzymes by
Thermostabilization and thermoattivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., A., Hayatsu, N., Fukuda, S., Fukunishi, Y., Funayama, T., Hara Kikuchi, N., Kojima, Y., Matsuyama, T., Itoh, M., Izawa, M., Kawai, J., Sato, K., Shibata, Y., Matsuyama, T., Nilsuma, H., Oda, H., Owa, C., Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Muramatsu, M., Okazaki, Y. and Hayashizaki, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Science Laboratory
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AV032131 Mus musculus adult C57BL/6J cerebellum Mus musculus cDNA clone 1500034B23, mRNA sequence.
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/clone_lib="Mus_musculus_adult_C57BL/6J cerebellum"
35 c 67 g 101 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Mus musculus"
                                                                                                                                 GI:3388927
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95.0%;
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Search completed: August 1, 2003, 20:43:07 Job time: 69.4754 secs
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                                                                                                                                                 Query Match 92.0%; Score 18.4; DB 28; Length 328; Best Local Similarity 95.0%; Pred. No. 1.4e+04; Matches 19; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2255 row: G column: 19
Class BAC ends
High quality sequence stop: 328.
Location/Qualifiers
                                                                              Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589 10449764
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hood, L.
                                                                                                                                                                                                                                                                 102
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                                                                                                                                                                                                                                                           /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
a 63 c 50 g 113 t
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
|mol type="genomic DNA"
|db_xref="taxon:9606"
|clone="plate=2255 Col=19 Row=G"
|sex="male"
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                            Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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20
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Match
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Copyright (c) 1993 - 2003 Compugen
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645
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AAA75620
AAS20735
ABL22726
ABL27256
ABL14642
ABL32039
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                                                                                                SUMMARIES
                                                                          Description
                         Drosophila melanog
Drosophila melanog
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Human cancer relat
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Human zalphall Lig
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## ALIGNMENTS

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AAS20735/c
ID AAS2077
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DT 09-APR
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Human :
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Cytoki
KW Cytoki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents part of the human zalphall ligand gene. C Zalphall ligand is a cytokine. The zalphall ligand is useful for Stalphall ligand is the proliferation and development of haematopoietic cells in vitro and in vivo. Zalphall ligand polynucleotides can be used as C primers or probes for cloning the zalphall gene. The zalphall ligand is C cuseful for treating tumourigenesis. A zalphall ligand-saporin fusion C cusin may be used for treating leukaemias and lymphomas. Antagonists C characterizing ligand-receptor interaction. Antagonists are also useful C control in thibiting expansion, proliferation, activation and differentiation C for inhibiting expansion, proliferation, activation and differentiation C for cells involved in regulating hematopoiesis. The zalphall ligand may c virus, a parasite or a bacterium. The zalphall polypeptides, antagonists, agonists and antibodies are also useful C for the detection, diagnosis, prevention, and treatment of diseases c associated with a zalphall ligand genetic defect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                                                                  09-MAR-2000; 2000US-0522217
                                                                                                                                       US6307024-B1
                                                                                                      23-OCT-2001.
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                            Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; B-cell proliferation; anti-tumour response; immune system;
                                                                                                                                                                                                                                                                             Human zalphall Ligand gene partial intron 3-partial exon 5 sequence
                                                                                                                                                                                                 immunostimulant; cytostatic; human; ds.
                                                                                                                                                                                                                                                                                                                      09-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     AAS20735 standard; DNA; 645 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 645 BP; 244 A; 107 C; 89 G; 204 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of haematopoietic cells in vitro and in vivo, and for treating tumourigenesis -
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11-MAR-1999;
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                   99US-123547P.
99US-123904P.
   99US-142013P
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99US-0265992.
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95.0%;
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Dillon SR,
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Hammond AK;
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ABL22726/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                             23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                               23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                              (PEKE ) PE CORP NY.
                                                                                                                                                                     27-SEP-2001.
                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                  pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 19651.
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                                                                                                                                                                                                                                                                                                                                                                                           ABL22726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of a novel cytokine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 52; Column 187-188; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 AATGTTTCTTAAAATTTTTT 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.0%;
95.0%;
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Dillon SR,
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Hammond AK;
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Adams M,

Li PWD,

Myers EW;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 33241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical; gene; ds
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceuticalidrugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                               11-JUL-2000; 2000US-0614150
                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                            Claim 1; SEQ ID NO 33241; 21pp + Sequence Listing; English.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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Matches
                       Query Match
             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 38408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                p-PSDB; ABB70539
                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 38408; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
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                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                    Sequence 4839 BP; 1360 A; 1051 C; 1092 G; 1336 T; 0 other;
                                                                               at ftp.wipo.int/pub/published_pct_sequences.
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  19;
              Similarity
                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
    Conservative
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95.0%;
                92.0%; Score 18.4; DB 23; 95.0%; Pred. No. 2.5e+02;
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    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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                                      Length 4839;
             Indels
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ABL32039
        06-OCT-2000
                                                          AAC29641;
                                                                                            AAC29641 standard; cDNA; 149 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders including eye diseases such as retinopathy, neovascular glaucoma and leukaemiá, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, the present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6164 BP; 1716 A; 134 C; 1458 G; 2855 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 12; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-130909/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002 (first entry)
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                                                                                                                                                                                                                            4643 AATGITTTTTAAGATTTTTT 4662
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                              AATGTTTCTTAAGATTTTTT 20
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                                                                                                                                                                                                                                                                                                                                         Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                  92.0%; Score 18.4; DB 24; 95.0%; Pred. No. 2.5e+02;
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                        21-FEB-2002
                                                                            WO200214500-A2
                                                                                                                                   Homo sapiens.
                                                                                                                                                           Human; cytostatic; gene expression; gene mapping; tissue profiling; gene therapy; cancer; tumour; gene; ss.
                                                                                                                                                                                                                                                    Human cancer related polynucleotide SEQ ID NO 3511.
                                                                                                                                                                                                                                                                                                                                      28-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABN63544 standard; cDNA; 556 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively total human RNAs or polyAt RNAs derived from 30 different tissues. Est of the mRNA because they are often obtained from oligo-dr primed cDNA derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' URR is rarely included. S' ESTs are derived from the 5' ends of mRNAs and even in those cases where longer 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                             ABN63544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-500381/45.
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94.7%;
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16-AUG-2001; 2001WO-US25840

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RESULT 9
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Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escobedo J, Garcia PD, Sudduth-Klinger J, Lamson G, Scott EM, Zhang G, Kassam A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR )
(HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus polynucleotide SEQ ID NO 10943.
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                                                                                                                                                                                                        27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2002.
                                                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                    (CHIR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 ATGTTTCTTAAGATTCTTT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                 CHIRON SPA
                                                                                                                     INST GENOMIC RES
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94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17.4; DB 24; Length Pred. No. 6.6e+02;
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Telford J, Tettelin H;

Masignani V,

Margarit Ros YI,

Grandi

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Fraser C;

P-PSDB; ABP25856 WPI; 2002-352536/38

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RESULT 10
ABN66487/c
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Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a biological sample. (I) are used to detect of acidencoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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Best Local (
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                                                                                                                                                                    27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                        Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 954 BP; 293 A; 145 C; 217 G; 299 T; 0 other;
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P-PSDB; ABP30884.
                                                                                                                                                                                                                                                                                                                                        Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus polynucleotide SEQ ID NO 887.
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                                                                                  Telford J,
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                                                                  l'ettelin
                                                                                                                  (CHIR-)
                                                                                                                                                                                                                                      29-OCT-2001; 2001WO-GB04789
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                                                                                                                  CHIRON SPA
                                                                                Masignani V,
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                                                                                                                    GENOMIC RES
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94.7%;
                                                                                  Margarit Ros YI,
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Pred. No. 6.5e+02;
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RESULT 11
ABM66079/c
ID ABM660
XX ABM660
XX Strept
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CC (Streptococcus pyogenes), comprising one of 5483 sequences (61), given in CC the specification. The proteins have antibacterial and antinflammatory CC activity. (I), nucleic acids encoding (I), ABM66044-ABM71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for CC the treatment or prevention of infection or disease caused by CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptococcus in a CC biological sample. (I) is used to detectmine whether a compound binds to CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to a vaccine or diagnostic composition. The disease caused by CC streptococcus that is prevented or treated may be meningitis. Nucleic CC acid encoding (I) may be used to recombinantly produce (I) and may be used to gene therapy. Antibodies to (I) are used for affinity CC chromatography, immunoassays, and distinguishing/identifying
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New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus polynucleotide SEQ ID NO 71.
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                                                                                                                                                                                                                                                                                                                           (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
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                                                                                                                                   2002-352536/38
DB; ABP25448.
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                                                                                                                                                                                                                                                             Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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94.7%;
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XX 15-JU
PR 12-JU
PR 17-JU
PR 17-JU
PR 11-OC
PR 11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                           10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                        New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                             WPI; 1999-132448/11.
                                                                                                                                                                                                                                                               Chen Y,
                                                                                                                                                                                                                                 Pfreundschuh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998;
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                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
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17-JUL-1997;
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97US-0896164.
97US-0061599.
97US-0061765.
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97GB-0021697.
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Sahin U,
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94.7%;
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Pred. No. 6.
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RESULT 13
ABK84789
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                                                                                                         Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                         WPI; 2002-435328/46.
                                                                                                                                                                                                                    Beazer-Barclay Y, Weissman SM, Yamaga S,
                                                                                                                                                                                                                                                                                              03-OCT-2000; 2000US-237189P
                                                                                                                                                                                                                                                                                                                                03-OCT-2001; 2001WO-US30821.
                                                                                                                                                                                                                                                                                                                                                                     11-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                      WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an anjagent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule, and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA differentially expressed in granulocytic cells #1360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1528 BP; 481 A; 308 C; 319 G; 420 T; 0 other;
                                                                                                                                                                                                                                                           (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK84789 standard; cDNA; 1528 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 67; Page 480; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 AATTTTTCTTAAGATTTTT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 88; granulocytic cell; DNA chip; bacterial infection; infection; parasitic infection; protozoal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AATGTTTCTTAAGATTTTT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 17.4; DB 20; 94.7%; Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                    Vockley
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identif DNA chip analysis as given in the specification, and comparing

(Gs) identified by

Claim 1; SEQ ID No 1360; 114pp; English.

toxicity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, by detecting the control the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (c) the level of expression of the gene is indicative of inflammation; (c) an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease; by contacting a tissue having considerably in an inflammation (especially chronic) or in a tissue, and for modulating GA; MA is useful for detecting a tissue having condulating GA; MA is useful for detecting a tissue of modulating GCA; was useful for sterening an agent capable of modulating GCA; was useful for expression of gene(s) conflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, RADS, adult respiratory distress syndrome. CC inflammatory bowel disease, Crohn's disease, ulcerative colities, conflammatic infection, protozoal infection, fungal infection and M5 is equence represents a gene differentially expressed in granulocytes. CC wote: The sequence data for this patent did not form part conformat directly from MIPO at the printed specification, but was obtained in electronic cf. figure of the printed specification, but was obtained in electronic cf. figure of the promote of the subject sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                          Venter JC,
                                                                                                                                                                                23-MAR-2000;
                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                               27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genomic polynucleotide SEQ ID NO 1981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL16836 standard; DNA; 2483 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (MA) an inflammation (especially beautiful and the state of the content of the conten
                                                                                      (PEKE ) PE CORP NY
                                                                                                                                                  11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1528 BP; 481 A; 308 C; 319 G; 420 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                       Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                               2000US-191637P
2000US-0614150
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94.7%;
                    Li PWD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.3e+02;
                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening (M3)
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WPI; 2001-656860/75

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 28268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2483 BP; 787 A; 474 C; 454 G; 768 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1981; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL11262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL11262 standard; cDNA; 2531 BP
                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                       Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
                                                                                          Claim 1; SEQ ID NO 28268; 21pp + Sequence Listing; English.
                                                                                                                                                                                            P-PSDB; ABB67159.
                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
insectivides, therapeutics and pharmaceutical drugs. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2339 AAGTTTCTTAAGATTTTT 2357
                                                                                                                                                                                                           2001-656860/75.
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                                                                                                                                                                                                                                             PWD,
                                                                                                                                              detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                 discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                     Sequence 2531 BP; 748 A; 489 C; 587 G; 707 T; 0 other;
                                                                                                                          Local
                                           2253 AATGTTTCTTAAGGTTTTT 2271
                                                                                                         18;
                                                                         1 AATGTTTCTTAAGATTTTT 19
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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"WILLIAMEN" APPLICATIONS NAM:

(cgn2 6/prodata/1/pubpna/USO7 NEW PUB.seq:*

(cgn2 6/prodata/1/pubpna/VCT NEW PUB.seq:*

(cgn2 6/prodata/1/pubpna/USO6 NEW PUB.seq:*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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13 US-10-027-632-200121	13 US-10-027-632-229994	9 US-09-811-284-104	10 US-09-764-677 10 US-09-960-352-13025 11 US-09-918-995-21175	9 US-09-834-291-28	US-09-834-291-14	.4 US-10-23-72 .3 US-10-027-632-224463 .5 US-10-027-632-21892	US-09-834-291-15   0 US-09-923-246-108	1
sequence 200121,	Sequence 239669,	Sequence 245649,	Sequence 13025, A Sequence 21175, A	Sequence 28, Appl Sequence 455, App	sequence 14, Appl sequence 20, Appl	Sequence 224463, Sequence 21892, A	Sequence 108, App Sequence 108, App	Description

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US-10-027-632-135562 US-10-027-632-354588 US-10-027-632-55212 US-10-027-632-84724 US-10-027-632-84724 US-09-938-842A-4583	US-09-833-381-1375 US-09-833-381-1375 US-10-066-543-2878 US-10-027-632-193079 US-10-027-632-135561	US-109-790-900-1 US-10-067-514-1 US-09-834-975-358 US-09-818-995-17530	<b>G</b> (	US-10-027-632-203400 US-09-938-842A-3068 US-10-114-170-126 US-09-834-291-4	US-10-027-632-1/0396 US-10-027-632-121985 US-10-027-632-9152 US-09-815-242-7222	US-10-027-632-256867 US-10-027-632-256868 US-10-027-632-256869 US-10-027-632-256870 US-10-027-632-256871
Sequence 30458, Sequence 304581, Sequence 255212, Sequence 84724, A Sequence 4583, Ap	Sequence 13/5, Ap Sequence 2878, Ap Sequence 193079, Sequence 135561,	. 351 175	Sequence 1, Appl Sequence 72, Appl Sequence 2928, Ap Sequence 1, Appli	שָׁיִבְ בְּיָּ		Sequence 256867, Sequence 256868, Sequence 256869, Sequence 256870, Sequence 256871, Sequence 170398,

## ALIGNMENTS

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TITLE OF INVENTION: 953 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-16
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US-09-834-291-15

US-09-834-291-15

US-09-834-291-15

Patent No. US20020042064A1

Patent NOORMATION:

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo Sapiens US-09-834-291-15
RESULT 2
US-09-923-246-108/c
US-09-923-246-108, Application US/09923246
; Sequence 108, Application US/09923246
; Patent NO. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: NO. US20020128446A1ak, Julia E.
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                        1 AATGTTTCTTAAGATTTTT 20
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100.0%; Pred. No. 43;
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Gaps

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CURRENT APPLICATION NUMBER: US/10/295,723

PRIOR APPLICATION NUMBER: 09/522,217

PRIOR APPLICATION NUMBER: 09/522,217

PRIOR APPLICATION NUMBER: US 60/123,547

PRIOR APPLICATION NUMBER: US 60/123,547

PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: US 60/142,013

PRIOR PILING DATE: 1999-07-01
                                           SEQ ID NO 108
LENGTH: 645
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Publication No. US20030125524A1
GENERAL INFORMATION:
APPLICANT: NO. US20030125524A1ak, Julia E.
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
ORGANISM; Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/923,246

CURRENT APPLICATION NUMBER: US/09/923,246

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

RIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

SOFTWARE: FASESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n = A,T,C or G
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TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
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                                                                     FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                    Holly, Richard D. Gross, Jane A. Johnston, Janet V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presnell, Scott R. Sprecher, Cindy A. Foster, Donald C.
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Dillon, Stacey R.
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Sequence 21892, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: US/0/218,006
PRIOR PILING DATE: 2002-07-12
PRIOR PILING DATE: 2002-07-12
PRIOR PILING DATE: 2002-07-12
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR TILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1090-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSI
SEQ ID NO 224463
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LOCATION: (1)...(587)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 224463, App
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KBY: misc feature
LOCATION: (1)...(645)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                       134 ATGTTTCTTAAGATTTTT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/146,002 FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                              2 ATGTTTCTTAAGATTTTT 19
                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           David G.
                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 18; DB 13; Length 587; 100.0%; Pred. No. 4.1e+02; ative 0; Mismatches 0; Indels
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Pred. No. 2.9e+02;
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1999-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
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US-09-834-291-20
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LENGTH: 733
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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR PRIOR PRICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 14
                                                                                                                                            Sequence 20, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION UMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 20
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/146,002
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8; DB 9; Length 20; Pred. No. 8.1e+02;
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; ORGANISM: Homo Sapiens US-09-834-291-20
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US-09-834-291-28
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/0343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC005

FURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                   ; Sequence 455, Application US/09764877; Patent No. US20020147140A1
                                                                                                                                                                                                                                                                                                                          US-09-764-877-455/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 28
LENGTH: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/09834291
Patent No. US20020042064A1
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
                                                                                     Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 32
NAME/KEY: SITE
                  FEATURE:
                                    ORGANISM: Homo sapiens
                                                      TYPE: DNA
                                                                      LENGTH:
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                                                                           366
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US-09-918-995-21175/c
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                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 21175
LENGTH: 479
                                                                                                                                    APPLICATION: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
NUMBER OF SEQ ID NOS: 38054
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Publication No. US20030073623A1
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SEQ ID NO 13025
LENGTH: 450
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APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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                 PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(479)
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OTHER INECRMATION: n = A,T,C or G
                                                                       ORGANISM: Homo sapiens
                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 56-BOVMS1-023-Q1-E1-F8
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LOCATION: (313)
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LOCATION: (310)
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Pred. No. 1
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Pred. No. 1.
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US-10-027-632-245649/c
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                       Sequence 245649, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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CURRENT APPLICATION NUMBER: US/10/027,632
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PRIOR APPLICATION NUMBER: 60/192,916
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 60/192,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,935
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PRIOR APPLICATION NUMBER: 60/189,960
PRIOR FILING DATE: 2000-03-16
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CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,783
PRIOR FILING DATE: 2000-03-16
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: 60/192,945
PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: No.
FILE REFERENCE: 00167US1
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PRIOR FILING DATE: 2000-03-16
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                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/192,234
FILING DATE: 2000-03-27
APPLICATION NUMBER: 60/192,155
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FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                  84.0%; Score 16.8; DB 9; Length 515; 90.0%; Pred. No. 1.2e+03;
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90.0%;
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Pred. No. 1.2e+03;
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2002-04-30

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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 229994
LENGTH: 583
TYPE: DNA
ORGANISM: Human
US-10-027-632-229994
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29
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SEQ ID NO 245649
LENGTH: 578
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Best Local Similarity
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                                                                                                            Query Match
Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
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90.0%; Pred. No. 1.
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 239669
LENGTH: 603
TYPE: DNA
TYPE: DNA
TYPE: DNA
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, NAME/KEY: misc feature
; LOCATION: (1)...(603)
; OTHER INFORMATION: n = A,T,C or
US-10-027-632-239669
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PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 239669, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                           Matches
                                                                                               Best
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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nes 18; Conserv
262 AATGTTTCCTAGGATTTTTT
                       1 AATGTTTCTTAAGATTTTTT 20
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Search completed: August 1, 2003, 13:37:02 Job time : 6.18607 secs

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Result
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Maximum Match 100%
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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-507-455-2

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US-08-507-455-2

US-08-507-455-2

US-08-920-422-17

US-08-920-422-17

US-08-920-422-17

US-08-920-32A-1250

US-09-107-532A-1250

US-09-108-115-1

US-09-092-508-15

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Sequence 108, App Sequence 126, App Sequence 146, App Sequence 146, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 2, Appli Sequence 17, Appli Sequence 1, Appli Sequence 15, Appli Sequence 165, Appli Sequence 165
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RESULT 2 US-09-453-702B-126/c ; Sequence 126, Application US/09453702B ; Patent No. 6365723

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GENERAL INFORMATION:

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Patent No. 6265157
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                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                    APPLICANT:
                                                           APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORKKO, JARMO
APPLICANT: KORKKO, JERNA
APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 53701-2113

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
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TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1176 AATGTGTCTTATGATTTTTT 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
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ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blattner, Frederick R. Burland, Valerie
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SEREDA, LARISA
                                                                                                                                                                                                                                                                    SPOTILA,
                                                                                                                                                                                     PACK, MICHAEL
                                                                                                                                                                                                                                                                      PROCKOP, DARWIN J. SPOTILA, LORETTA D.
                                                                                                                                                                                                            LARSON, ANDREA W.
    PANITCH SCHWARZE JACOBS & NADEL, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plunkett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251-9166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.8; DB 4; Length 2272; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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US-09-205-258-154
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 154, App. Patent No. 652517
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Young et al. TITLE OF INVENTION: 207 Human Secreted Proteins
                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/205,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 146:
                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 60/048,885
                                                                                             EARLIER
                                                                                                             EARLIER
                                                                                                                                   EARLIER
                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEPHAX: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D.,
REGISTRATION NUMBER: 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/212,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
               APPLICATION NUMBER: 60/049,020 FILING DATE: 1997-06-06
                                                     APPLICATION NUMBER: 60/048,880 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,896 FILING DATE: 1997-06-06
                                                                                                                                   FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 TGTTTCTTAAGATTTTAT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
APPLICATION NUMBER: 60/048,876
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                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09205258
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Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
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US-09-205-258-154
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
                                                                                                   SEQ ID NO 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/049,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARLIER FILING DATE: 1997-06-06
PARLIER APPLICATION NUMBER: 60/049,373
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER APPLICATION NUMBER: 60/048,974
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                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER
                                                                                                                                                                                                                         EARLIER FILING DATE: 1998-07-15
                                                                                                                                                   WUMBER OF SEQ ID NOS: 1227
                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                        ENGTH: 2388
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,019
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,972 FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,883
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/048,878
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/048,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/048,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/048,962
                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-06-06
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                                                                                                                              PatentIn Ver.
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Query Match

82.0%; Score 16.4;

DB 4;

Length 2388;

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                                                                                                                                    Matches
                                                                                                                                                                                             Query Match
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
ADDRESSEE: PANITCH SCHWARZE, 2005 MARKET STREET, 22ND
STREET: ONE COMMERCE SQUARE, 2005 MARKET
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: V. ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
NAME: DOYLE LEARY Ph.D., KATHRYN
NAME: DOYLE LEARY Ph.D., CATHRYN
NAME: DOYLE LEARY Ph.D., KATHRYN
NAME: DOYLE LEARY Ph.D., CATHRYN
NAME: DOYLE LEARY PH.D., CA
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PRIOR APPLICATION NUMBER: US 08/212,322
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 24183 base pai
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 14-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                             Local Similarity
   20352 TGTTTCTTAAGATTTTAT 20369
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                                          .3 TGTTTCTTAAGATTTTTT 20
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SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEEEDA, LARISA
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EARLY, JAMES
KORKKO, JARMO
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                                                                                                                                       Conservative
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                                                                                                                                                                       82.0%; Score 16.4; DB 3; Length 24183; 94.4%; Pred. No. 1.9e+02;
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                       NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
                                                              NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a,
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TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
                                                                                                        NAME/KEY: misc feature
LOCATION: (191989) .. (191989)
OTHER INFORMATION: n equals a,
                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (163385)...(163385)
OTHER INFORMATION: n equals a,
    LOCATION:
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LOCATION: (148948) .. (148948)
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (98343) ... (98343)
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LOCATION: (98239)
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LOCATION: (98159)...(98159)
OTHER INFORMATION: n equals a,
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LOCATION: (98120)...(98120)
OTHER INFORMATION: n equals a,
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PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
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TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6503729
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature LOCATION: (1096846)...(1096846) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (871619)...(871619) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc\_feature LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, 71h.... NAME/KEY: misc feature γονττοΝ: (1084830)...(1084830) NAME/KEY: misc feature LOCATION: (85533)..(855539) OTHER INFORMATION: n equals a, LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, LOCATION: (779455)...(779455)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (682442)..(682442) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (657203)..(657203) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (674435) .. (674435) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (622708)..(622708) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (600992)..(600992) OTHER INFORMATION: m equals a, LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature
COCATION: (559167)..(559167) NAME/KEY: misc\_feature
rocation: (319226)..(319226) OTHER INFORMATION: n equals a, LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature OTHER INFORMATION: n equals a, LOCATION: (309418) .. (309418)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (309398)..(309398) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (234814)...(234814) OTHER INFORMATION: n equals OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (234220)...(234220) OTHER INFORMATION: n equals INFORMATION: n equals a, (713652) .. (713652) (234220)..(234220) feature reature reature teature feature reature feature feature n equals a, )..(312837) ŗ t, c, ţ, 9 a, ŗ ŗ Ĺţ ŗ , ŗ ŗ , ŗ ຸດ ŗ ů Ĺ . ņ ņ 'n ņ ņ 'n ú ņ ç ņ 'n ņ 읁 õ or Ö 유 ņ ç 'n ç or 0 F or or P ç or g ဝူ or g ç ç 유 ę, or g or g or g ω ç ω ω g

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US-08-916-421B-1
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                                                                                                                                                                                                                                                                                              ; TYPE: DNA ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-1361
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APPLICANT: LYIND DOUGETC-Stamm et al
APPLICANT: LYIND DOUGETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 1997-007

CURRENT APPLICATION UNMER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1361
LENGTH: 672
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LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a,
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LOCATION: (1313224)...(1313224)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1130881)..(1130881)
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (1470091)...(1470091)
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LOCATION: (1349473)..(1349473)
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Similarity 89.5%;
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                                                                                                                                                                                    Score 15.8; DB 4; Length 672; Pred. No. 3.9e+02;
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RESULT 8
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; Patent No. 5695961
; GENERAL INFORMATION:
                                                              US-08-507-455-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO:
                             Query Match
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/507,455
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MEDIUM TYPE: Floppy disk
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LENGTH: 1619 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,0
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APPLICATION NUMBER:
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NAME/KEY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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79.0%; Score 15.8; DB 1; Length 1619; Local Similarity 89.5%; Pred. No. 3.7e+02; hes 17; Conservative 0. Miamor-Live
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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1035..1036
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692..697
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668..673
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574..579
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; RELEVANT RESIDUES IN SEQ ID NO: US-08-759-436-4
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US-08-759-436-4/c
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INFORMATION FOR SEQ ID NO: 4:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,436
FILING DATE: 5-Dec-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 212-708-1935
                                 ¿DATE: december-1995
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MEDIUM TYPE: Floppy COMPUTER: IBM PC com
                                                                                                                                                                            AUTHORS:
                                                PAGES:
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                                                                                                   AUTHORS: Pereira, Andy
TITLE: Molecular characterization of the CER1 gene
TITLE: of Arabidopsis involved in epicuticular wax
TITLE: biosynthesis and pollen fertility
JOURNAL: Plant Cell
                                                                                                                                                                                                                                                                                  MAP POSITION:
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                                                                                                                                                                                                                                                                                                                                            LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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REGISTRATION NUMBER: 33,778
REFERENCE/DOCKET NUMBER: U011063-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: New York
STATE: New York
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Keijzer, Christian J.
Stiekema, Willem J.
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US-08-507-455-2
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                                                           Query Match
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Best Local Similarity 89.5%;
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HYPOTHETICAL: N
ANTI-SENSE: NO
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FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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NUMBER OF SEQUENCES:
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                                                                                                                   NAME/KEY:
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TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 08-SEP-1995
CLASSIFICATION: 435
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                                           Similarity
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                             Conservative
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                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                             double
                                         79.0%;
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                            0; Mismatches
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                                     Score 15.8; DB 1;
Pred. No. 3.7e+02;
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                                                  Length 1754;
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                       Gaps
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1397 AATGATTATTAAGATTTTT 1415

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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/48,725
PRIOR APPLICATION NUMBER: 09/48,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt FL genes Version 1.0
SEQ ID NO 616
LENGTH: 3084
                                                                                                                                                                                                                                                                                                                                                                                                   밁
; TYPE: DNA
; ORGANISM: Mus musculus
US-08-920-422-17
                                                                                                                                                                                                                                                                                                                         US-08-920-422-17
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                                                                                                                                                                                                                                                            Patent No. 6255473
GENERAL INFORMATION:
                                                                         SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 17
                                                                                                                                                                                                                                                                                    Sequence 17, Application US/08920422A Patent No. 6255473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                   APPLICANT: Vitek, Michael P.
APPLICANT: Mitsuda, No. 625473iaki
APPLICANT: ROSES, Allen D.
TITLE OF INVENTION: Presentlin-1 Gene Promoter
FILE REFERENCE: VITEKPRESENILIN
CURRENT APPLICATION UNMBER: US/08/920,422A
CURRENT FILING DATE: 1997-08-29
AUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (633)..(1883)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                         ENGTH: 48974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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1 Similarity 89.5%;
17; Conservation
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Xue, Aidong J.
Yang, Yonghong
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Ren, Feiyan
Chen, Rui-hong
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Zhou, Ping
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Wehrman, Tom
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Pred. No. 3.
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; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-545-528D-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3414, Application US/09107532A
PATENT NO. 6583275
PATENT NO. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6537773
TITLE OF INVENTION: Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08545528D Patent No. 6537773
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/545,528D CURRENT FILING DATE: 1995-10-19 PRIOR APPLICATION NUMBER: US 08/488,018 PRIOR FILING DATE: 1995-06-07 PRIOR APPLICATION NUMBER: US 08/473,545 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fraser et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 580073
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                  APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                              APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RO
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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                                                                                                                                                                                                         OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 3e+02;
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Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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INFORMATION FOR SEQ ID NO: 3414: SEQUENCE CHARACTERISTICS:

FEATURE:

ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

HYPOTHETICAL: NO ANTI-SENSE: NO

TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)

LENGTH: 339 base pairs TYPE: nucleic acid STRANDEDNESS: double REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
TELEFAX: (781)893-8277

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; LOCATION: (B) LOCATION 1...339; 
; SEQUENCE DESCRIPTION: SEQ ID NO: 3414: 
US-09-107-532A-3414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-107-532A-1250/c
         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELEPHONE: (781)893-5007

TELEPAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 1250:

SEQUENCE CHARACTERISTICS:

LENGTH: 1020 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1250, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

APPLICANT: Lynn A DOUCETIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 AATGITTCTTATGATTT 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.0%;
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Search completed: August Job time: 4.65066 secs
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                                                                                                                                             Matches
                                                                                                                                                                               Query Match
                                                                                                                                                              y Match 77.0%; Score 15.4; DB 4; Local Similarity 94.1%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1020
SEQUENCE DESCRIPTION: SEQ ID NO: 1250:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                          FEATURE:
                                                                       201 AATGTTTCTTATGATTT 185
                                                                                                         1 AATGTTTCTTAAGATTT 17
                                                                                                                                           16; Conservative
               1, 2003, 08:37:20
                                                                                                                                             0
                                                                                                                                               Mismatches
                                                                                                                                                                               Length 1020;
                                                                                                                                               Indels
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<u>.</u>

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compus

Compugen Ltd.

Run on:

August 1, 2003, 08:37:27; Search time 78.1573 Seconds (without alignments) 10468.541 Million cell updates/sec

Title: Perfect score:

Sequence: Scoring table:

IDENTITY\_NUC Gapext 1.0

1 ggacaagccctgacaagcca 20

US-09-834-291-24

2888711 seqs, 20454813386 residues

5777422

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

GenEmbl:\*

gb ba: \*
gb htg: \*
gb in: \*
gb om: \*
gb ov: \*
gb pat: \*
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em pat:\*
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Total number of hits satisfying chosen parameters:

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1 AXO26093 LOCUS INTION DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	Result NO.  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	<b>.</b>
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AX026093 Sequence 5 AX026093 AX026093.1 Homo sapier Homo sapier Eukaryota; Mammalia; 1 1 1 1 1 Novel reces substances	March 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 92.0 92.0 92.0 92.0 92.0 92.0 92.0	م الم
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GI:10187524 GI:10187524 g (human) g (human) Metazoa; Cho utheria; Pri utheria; Man potentially	συννικου και	
20 h 1t DE19847 524 524 Chordata; Primates; Primates; Krammer , Krammer , Krammer	AX026093 AX026120 AX026120 AX026120 AX026120 AX026091 AX026091 AX026092 AX026092 AX026092 AX026093 AX026094 AL157394 AX1356352 AC11499 AC11499 AC011499 AC011499 AC011499 AC011499 AC11529259 AC139977 AL929559 AC12589763 AC125884 AC1127943 AC125886 AC125886 AC1258871 AC125887 AC126897 AC126897 AC1268975 AC1268976 AC1268976 AC1268976 AC1268976 AC1268976 AC1268976 AC1268976 AC1268976 AC1268976 AC1268978	
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31: em\_htg\_inv:\*
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33: em\_htg\_pin:\*
34: em\_htg\_pin:\*
35: em\_htg\_roi:\*
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                                  Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19847779-C 24 03-FBB-2000;
DEUTSCHES KREBSFORSCH (DE)
                                                                                                          Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                       Sequence 24 from Patent DE19847779.
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Novel receptor dna useful for identifying apoptosis-modulating
substances potentially useful for cancer chemotherapy
Patent: DE 19447779-C 10 03-FEB-2000,
DEUTSCHES KREBSFORSCH (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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mol_type="genomic DNA"
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mol_type="genomic DNA"
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Direct Submission
Submitted (08-SEP-1998) Mueller M., Department of Internal Medicine
IV, University Hospital, Bergheimerstr. 58, Heidelberg, 69115,
                                                                                                                                                                                                                                                                                                                                                                                                160 GGÁCAAGCCTGÁCAAGCCA 179
                                                                 Mueller, M.
                                                                                               p53 activates the CD95 (APO-1/Fas) gene in response to DNA damage by anticancer drugs
J. Exp. Med. 188 (11), 2033-2045 (1998)
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                                                                                                                                              Mueller, M.; Wilder, S., Bannasch, D., Israeli, D., Lehlbach, K., Li-Weber, M., Friedman, S.L., Galle, P.R., Stremmel, W., Oren, M. and Krammer, P.H.
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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266 bp DNA linear
Homo sapiens DNA for enhancer of CD95 gene, partial.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
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Novel receptor dna useful for identifying apoptosis-me substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 2 03-FEB-2000;
DEUTSCHES KREBSFORSCH (DE)
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                                                                                                                                                                               Sequence 3 from Patent DE19847779.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mueller-Schilling,M., Krammer,P. and Oren,M.
Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 3 03-FEB-2000;
                                                                                                               Homo sapiens
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                                                                                                                                  Homo sapiens (human)
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/db_xref="taxon:9606"
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72 c 110 g
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/mol_type="genomic DNA"
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181 c 216 g 18:
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Sequence 4 from Patent DE19847779.
AX026092
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Sequence 1 from Patent DE19847779.
AX026089
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
676 c 657 g 76
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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On Aug 31, 2001 this sequence version replaced gi:14161146. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
                                                                                                                                                               Submitted (22-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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AL157394
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/db_xref="taxon:9606"
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AX026094
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                                                                                                                                                                                                                                                                            Novel receptor dna useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy Patent: DE 19847779-C 6 03-FEB-2000; DEUTSCHES KREBSFORSCH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mueller-Schilling, M., Krammer, P. and Oren, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 6 from Patent DE19847779.
AX026094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 Ppl1 190010 is fer the KHGP/Chr10 Ppl1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP http://www.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
6 C 5 9
                                                                                                                                                                                                                                       Location/Qualifiers
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105808, .105972
/note="Sequence from AC015461 sequenced by WIBR."
105973, .105989
/note="Sequence confirmed by AC015461 sequenced by WIBR."
136398 c 36888 g 58358 t
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100157. .100198
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/clone_lib="RPCI-11.2"
100119. .100156
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
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TITLE
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19; Conserv
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 26% of reads Chemistry
Dye-terminator Big Dye; 73% of reads
Consensus quality: 159499 bases at least Q40
Consensus quality: 162148 bases at least Q20
Consensus quality: 163256 bases at least Q20
Consensus quality: 163926 bases at least Q20
Insert size: 165512; sum-of-contigs
Insert size: 206683; 10.2% error; agarose-fp
Quality coverage: 4.08x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (18-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 21, 2001 this sequence version replaced gi:12539659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: dJ859H16
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             coverage: 3.39x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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36206
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                                                                                                                                                     12019: contig of 12019 bp in length
12119: gap of 100 bp
32657: contig of 20538 bp in length
32757: gap of 100 bp
36105: contig of 3348 bp in length
36205: gap of 100 bp
41069: contig of 4864 bp in length
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73695:
83277:
83377:
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62497:
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51754:
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1: contig of 10485 bp in length
1: contig of 10643 bp in length
7: contig of 10643 bp in length
7: gap of 100 bp
5: contig of 11098 bp in length
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                gap of 100 bp
contig of 9582 bp in
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Pred. No. 4.5e+02;
0; Mismatches 1
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6, *** SE
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SEQUENCING IN
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101274
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fragment_chain:2"
101274. _103420
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/clone_lib="RPCI-5"
1. .12019
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                    /note="assembly_fragment:01704
fragment_chain:3"
                                                                                                                                                                                                                                                                                      83378. .9884
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                                    note="assembly_fragment:01435/
fragment_chain:3"
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fragment_chain:3"
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ragment_chain:2"
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ragment_chain:2"
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ragment_chain:2"
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fragment_chain:1"
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ragment_chain:1"
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ragment_chain:1"
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ragment_chain:1"
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note="assembly_fragment:00291"
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140183: contig of 1
140283: gap of 1
147703: contig of 1
147803: gap of 1
158100: contig of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158100: Contig of 10297 bp in length 158200: gap of 100 bp 161982: contig of 3782 bp in length 162082: gap of 100 bp 167412: contig of 5330 bp in length
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of 8623 bp in length
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100 bp
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REFERENCE
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 27, 2002 this sequence version replaced gi:24394955. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence dat from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                              During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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162083. .167412
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fragment_chain:5"
147804. .158100
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140284. .147703
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119728. .128350
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41224 c 42341 g 40447 t . 1
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128451. .140183
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|58201. .161982
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fragment_chain:5"
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Pred. No. 70;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clouerequest@sanger.ac.uk on Apr 2, 2003 this sequence version replaced gi.29134752. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data
                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 190946 bases at least Q40
Consensus quality: 191521 bases at least Q30
Consensus quality: 191867 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                        coverage: 8.09x in Q20 bases; agarose-fp
                                                                                                                                                                          Insert size: 192452; sum-of-contigs
Insert size: 197663; 4.4% error; agarose-fp
Quality coverage: 8.26x in Q20 bases; sum-of-contigs Quality
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For further details see http://www.chori.org/bacpac/home.htm
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 193352)
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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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/chromosome="X"
                                                             92.0%; Score 18.4; DB 2; Length 193352; 95.0%; Pred. No. 68; ative 0; Mismatches 1; Indels 0;
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BI763679 793 bp mRNA linear EST 25-SEP-2001 603049567F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5189752 5', mRNA sequence.
BI763679 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11474 row: e column: 17 1 (bases 1 to 793) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Contact: Robert Strausberg, Ph.D. 786.

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cgi-bin/cluster.gi?seq=CSODE002DG09QPl&cluster=5554.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5554.r For
more information about this cluster, see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 962)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Feb 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE002YN18
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/mol type="mRNA"
/mol type="mRNA"
/db_xref="raxon:9606"
/db_xref="raxon:9606"
/clone="IMAGE:5189752"
/clone="IMAGE:5189752"
/clone=lib="NHAGE:116"
/note="Organ: pooled colon, kidney, stomach; Vector:
/note="Organ: pooled colon, kidney, stomach; Vector:
/note="Organ: pooled colon, kidney, stomach; Vector:
/note="Organ: pooled colon; is colone, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                         Avenue Genoscope sequence ID : CSODE002DG09Qp1.
Location/Qualifiers
        /clone="CSODEGOZYN18"
/tissue type="PLACENTA"
/tissue type="PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Hib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecorv sites of the pCMVSPORT 6 vector.
Library was not normalized
                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001 this sequence version replaced gi:12871113.
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100.0%; Pred. No.
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Best Local Similarity
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM12796 row: 1 column: 21
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of units.
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AGENCOURT 6763280 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5756324
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//clone_lib="NIH_MGC_118"
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/db_xref="taxon:9606"
/clone="IMAGE:5756324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="leukocyte"/
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DEFINITION

W45225 486 bp mRNA linear EST 10zc23c09.rl Soares\_senescent\_fibroblasts\_NbHSF Homo sapiens

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COMMENT
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1 (bases 1 to 486)
1 (bases 1 to 486)
1 (lark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilsoh,R.
                                                                                                                                                                                                                                                                       265 GACAAGCCCTGACAAGCC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone IMAGE:323152 5' similar to gb:L25081 TRANSFORMING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 972 Sto
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 972 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
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                                                                                                                        TgESTzya24g01.y1 TgVEG118 Tachyzoite cDNA Library Toxoplasma gondii cDNA clone TgESTzya24g01.y1 5' similar to TR:Q63030 Q63030 RAT ALPHA-SMOOTH MUSCLE ACTIN MRNA FRAGMENT ;, mRNA sequence.
Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
                                                                                                                                                                               BG659530
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129 c 140 g 95 t 2 others
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/mol_type="mRNA"
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Contact David Sibley (toxoest@borcim.wustl.edu)
information relating to organism, libraries, or
Seg primer: -40RP from Gibco
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Fax: 314 286 1810
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BU142933
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Gallus gallus ___
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603135537F1 CSEQCHL25 Gallus gallus cDNA clone ChEST119i9 5', mRNA
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(bases 1 to 753)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
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/clone_Tib=TgVBG118 Tachyzoite cDNA Library"
/note=Tvector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI
/note=Tvector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI
/note=Tvector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI
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/dev_stage="Tachyzoite"
/lab_host="DH10B"
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0197 row: J column: 18
'Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 GGACAAGCCCTGACAAGC 179
                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
                                                                                                                                                                                                                    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                  plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 01612008930
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/lab_host="DH10B"
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        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0249 row: M column: 17
                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musil (bases 1 to 684)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                   Contact: Robert B. Weiss
                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                    plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ450876 684 bp DNA linear GSS 04-OCT-200 1M0249M17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0249M17 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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                                                                                                                                USA
                                                                                                                                     Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA
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strain="C57BL/6J"
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94.7%;
column: 17
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Location/Qualifiers
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                                                                                                                                                                                                              Humphray, S. J., Huckle, E. and Durham, J.L.

Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Submitted (26-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA; UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished humquery@sanger.ac.uk Unpublished This sequence was generated from the SP6 end of BAC 269M11. 269M11 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                               http://www.sanger.ac.uk/Projects/D_rerio/
                                                                                                                                                                                         Keygene. Further details:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hint end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwp2 (gil473214[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was amnealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10<sup>L</sup>Gold (Stratagene) cells and selected for ampicillin resistance."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                          /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-269M11"
                                                                              organism="Danio rerio"
                                                                                                                               Location/Qualifiers
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Pred. No. 7.3e+02;
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1 (bases 1 to 701)

Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z., Miao, G., Caraher, N. and Hanafey, M.K.

Dubont Wheat cDNA Sequence
Unnublished
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                                                                                                                                                                                                                                                                                                         18;
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Similarity 94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13.
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Danio rerio (zebrafish)
Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                          Danio rerio genomic clone DKEY-183M20, BX179961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 302-631-2602
Fax: 302-631-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Scott V. Tingey
                                                                                           BX179961.1 GI:28011764
                                                                                                                                            BX179961
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                                                                                                                                                                                                                                                                                                                                                                                           /clone="wr1.pk0046.e7"
/tissue_type="root"
/clone lib="wr1"
/clone = "wr1"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Wector: pBluescript SK+; Site_1: CoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Weath (Triticum aestivum L.) root; 7 day old
seedling, light grown"
a 188 c 131 g 156 t 27 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:4565"
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Pred. No. 7.4e+02;
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                                                                                                                                                                                                                                                        Seq primer: SK
                                                                                                                                                                                                                                                                                                                                                   Cambridge University
Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                     Clone information and library can be obtained from Jim Ajioka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgEST0074 TgRH Tachyzoite cDNA
5' end, mRNA secritoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GACAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                 Email:
                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toxoplasma gondii expressed sequence tags: insight into tachyzoite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wan, K.-L., Blackwell, J.M. and Ajioka, J.W.
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1 (bases 1 to 331)
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                        jwa@mole.bio.cam.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Ajioka JW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was generated from the SP6 end of BAC 183M20. 183M20. is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/D_rerio/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cypriniformes;
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                                                                                                                                                                                                                                                                                                               jajioka@hgmp.mrc.ac.uk
              /lab_host="XL1-Blue MRF/"
/clone_lib="TgRH_Tachyzoite_CDNA"
/note="Vettor: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
/note="Vettor: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
Toxoplasma RH strain tachyzoites were grown in human
foreskin fibroblast cultures in vitro. The library was
    constructed by K.L. Wan,
                                                                                                                       /db_xref="taxon:5811"
/clone="tgb008"
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                             strain="RH"
                                                                                                                                                                                            organism="Toxoplasma gondii"
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/note="vector pIndigoBAC-536"
150 c 151 g 235 t
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/clone="DKEY-183M20"
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                                                                                                                                                                               type="mRNA"
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94.7%;
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  Cambridge University.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0018 row: K column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 0018 row: K column: 23
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGACAAGCCCTGACAAG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 429)
Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ781046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inserts
                                                                                                                                                                                                                                                          /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42rv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                      clone="UUGC2M0018K23"
                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus'
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LINL; contact the IMAGE Consortium (infoeimage.llnl.gov) for further information. Insert Length: 1020 Std Error: 0.00 High quality sequence stop: 436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 531)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3', mRNA sequence.
AA195416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA195416 531 bp mRNA linear zr36f10.s1 Soares NhHMPu_S1 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                               /clone_lib="Soares NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHHJW) were made in vitro. Pollowing HAP purification, this DNA
were made in vitro. Pollowing HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-285223,
340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="Pooled human melanocyte,
                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:665515"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Homo sapiens"
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tive 0;
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Query Match

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Search completed: August Job time: 68.4754 secs

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AW131236/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E, Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 423.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW131236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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AW131236
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                                                                                                                                                                                                           /clone lib="NCI_CGAP_Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                         11549-011"
146 c
                                                                                                                                                                                                                                                                                                              /tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
                                                                                                                                                                                                                                                                                                                                                                            /db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                'lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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Pred. No. 1.3e+03;
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20
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| SIDS1/gcgdata/genseq/genseqn-emb1/NA1987.DAT: *
| SIDS1/gcgdata/genseq/genseqn-emb1/NA1987.DAT: *
| SIDS1/gcgdata/genseq/genseqn-emb1/NA198.DAT: *
| SIDS1/gcgdata/genseq/genseqn-emb1/NA198.DAT: *
| SIDS1/gcgdata/genseq/genseqn-emb1/NA199.DAT: *
| SIDS1/gcgdata/genseq/genseqn-emb1/NA2001.DAT: *
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Copyright (c) 1993 - 2003 Compugen
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_/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	8	7	σ	σı	.4	w	N	_	Result
	15.8	15.8	16	16.4	16.4	16.4	16.4	20	Score
	79.0	79.0	80.0	82.0	82.0	82.0	82.0	100.0	% Query Match
			433						Query Match Length DB ID
	25	25	25	25	22	25	25	21	DB BC
	ABZ41531	ABX27459	ABX52814	ABZ74552	AAK81012	ABZ74553	ABX91757	AAZ88700	ID
_	N. gonorrhoeae nuc	Human GDP-mannose	Bovine EST associa	Secreted protein g	Human immune/haema	Secreted protein g	Murine gene trappe	Human CD95 recepto	Description

Aspergillus fumiga		25	3604	77.0	15.4	45	
	ABT17900	25	3038	•	٠	44	
Human secreted pro	AACE	21	2059	77.0	15.4	43	Ω
Human secreted pro	AAC59	21	2010			42	a
	AAC79	21	1560	•		41	a
Human secreted pro	AAC93516	21	921			40	O
	ABX60	25	860			39	
encoding	ABX60548	25	860	77.0		ω 8	
n musculos		22	860		15.4	37	
Human musculoskele	AAL3	22	860	٠	15.4	36	
cDNA sequence #557	AAS627	24	845	•	15.4	35	a
	AAZ:	20	758		15.4	34	a
cDNA encoding nove		25	673			ω S	
Human musculoskele	AAL	22	673		•	32	
Streptococcus poly		24	498	77.0	•	31	
Human neuregulin-1	ABT01957	24	401	•		30	a
Human neuregulin-l		24	401	77.0	•	29	a
Human neureguin g		22	401	77.0	•	28	a
Human neuregulin g	AAK95694	22	401	٠	•	27	a
Bovine EST associa		25	272	•	15.4	26	
micu		22	_	•	15.8	25	C
		24	155074	•	15.8	24	
Human gene express		24	i		15.8	23	
nt gen		24	88421		15.8	22	
Human immune/haema		22	39325	79.0	15.8	21	a
Propionibacterium		23	16949	•	15.8	20	
C. glutamicum deri		25	1482	•	15.8	19	ი
C. glutamicum deri		25	1482	•		18	O
opionibacterium		23	1012	•	15.8	17	
Human immune/haema		22	750	•	15.8	16	
Human immune/haema	AAK74243	22	749	•	15.8	15	
Human immune/naema		22	749			14	
Human immune/haema		22	409	•	ū	13	
Neisseria gonorrho	AAZ1	20	381	•	ū	12	n
	AAZ531	21	309	•	15.8	ב	
	AAZ53178	22	288	•	ຫ	10	
	AAZ11974	20	273	•	5	9	Ω

## ALIGNMENTS

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RESULT 1
AAZ88700
IID AAZ88
XX AAZ8
AC AAZ8
XX Huma
DE Huma
XX Canc
XX Canc
XX Home
XX Canc
XX Oan
X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p53; CD95 receptor; human; screening; apoptosis-modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ88700 standard; DNA; 266 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CD95 receptor intron 1 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ88700;
                                                                                                                                                                                16-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer chemotherapy; ss.
Krammer P,
                                                                                                                                                                                                                                                                       16-OCT-1998;
                                                                                      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
    Mueller-Schilling M, Oren M;
                                                                                                                                                                                98DE-1047779
                                                                                                                                                                                                                                                                           98DE-1047779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 160..179
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/bound_moiety= p53
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RESULT 2
ABX91757/c
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Best Local S
Matches 20
     The present invention relates to novel murine cDNAs produced using gene trap technology. The OMNIBANK gene trapped sequences (GTSs) are individually identified novel genes, and are useful in functional genomic analysis, in the discovery and development of new therapeutic and diagnostic agents, for gene discovery, for diagnostic gene expression analysis, for cross species hybridiaation analysis, and for
                                                                                                                                                 New murine polynucleotides comprising gene trapped sequences, useful in functional genomic analysis, in the development of new therapeutic or diagnostic gene expression analysis or for
                                                                                                         Claim 2; SEQ ID NO 1101; 29pp; English.
 genetic_manipulations
                                                                                                                                           genetic
                                                                                                                                                                                                              WPI; 2003-288124/28.
                                                                                                                                                                                                                                                                                  (FRIE/)
                                                                                                                                                                                                                                                                                                                         01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene identification; functional genomic analysis; gene discover gene expression analysis; cross species hybridisation analysis; antisense inhibition; gene targeting; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine gene trapped sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                    30-NOV-2000; 2000US-0728444.
                                                                                                                                                                                                                                                                                                                                                                                                           US2002161207-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                       de snw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX91757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX91757 standard; cDNA;
                                                                                                                                                                                                                                                                    (SAND/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel p53-binding region of a human CD95 receptor DNA molecule. The p53-binding region, or a vector containing it, can be used to screen for apoptosis-modulating substances potentially useful for cancer chemotherapy. This sequence represents a fragment of the human CD95 receptor intron 1 which contains a p53 binding region described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel receptor DNA useful for identifying apoptosis-modulating substances potentially useful for cancer chemotherapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-162245/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Fig 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGACAAGCCCTGACAAGCCA 20
                                                                                                                                        manipulations
                                                                                                                                                                                                                                                                    SANDS
                                                                                                                                                                                                                                                                                             FRIEDRICH G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse; gene trap technology; gene trapped
                                                                                                                                                                                                                                                                  ZAMBROWICZ B.
SANDS A T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 BP; 49 A; 72 C; 110 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                         99US-168360P
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such as antisense inhibition
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                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                       Sands AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GTS) SEQ ID No 1101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 21;
Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence; GTS;
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           and for
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                               acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV; antianaemic; vulnerary; chromosome 15q24-25; gene: ds
                                                                                                                                                                                                                                                                                              27-MAR-2001; 2001US-278650P.
12-SEP-2001; 2001US-0950082.
12-SEP-2001; 2001US-0950083.
                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polynucleotides of the invention are also useful for isolating CDNAs, genomic clones or full-length genes/polynucleotides, or their homologues, heterologues, paralogues or orthologues, that are capable of hybridising to one or more of the new murine polynucleotide sequences. The polynucleotides are also useful for identifying the coding regions of the murine genome, and as hybridisation probes. ABX90657-ABX91862 represent the murine GTSs of the invention. Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                       WO200277013-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein gene 346 genomic fragment HTOHO21, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ74553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ74553 standard; DNA; 8243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 516 BP; 163 A; 90 C; 118 G; 140 T; 5 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein; cancer; tumour; hyperproliferative mune disorder; inflammation; angiogenic diseases; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site at seqdata.uspto.gov/psipsDIDEntry.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                  2002WO-US09370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%;
94.4%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516;
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ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted protein genes, and ABP00947-ABP01363 represent the proteins they encode ABZ73698-ABZ74687 represent human secreted protein genomic fragments. Tinvention also encompasses antibodies specific for the secreted protein the use of the secreted proteins in drug screening and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins are thought to be involved in biological activities associated with cellular signalling, cellular differentiation, cell migration, prohormone activation and neurotransmitter activity. The

proteins,

encode

nucleic acids encoding them, antibodies or antibody

New human secreted proteins and nucleic acids, useful for detecting treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia

WPI; Rosen

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Ruben SM;

2003-040578/03

Disclosure; Page 2282-2284; 2474pp; English.

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RESULT 4
AAK81012/c
ID AAK81012 standard; DNA; 12710 BP.
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Best Local S
Matches 17
                                                                                                                                                                                                       19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing or treating cancers or other hyperproliferative disorders. Additionally, the secreted proteins and their nucleic acids may also be used in the treatment of autoimmune disorders, inflammatory disorders, diseases involving angiogenesis, AIDS (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein genomic fragment referred to in the disclosure of the invention.
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic
cytostatic; gene therapy; vaccine; metastasis; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK81012;
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                                                                                                                                                                              07-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                      17-MAR-2000;
18-APR-2000;
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                                                                                                                                                                                          ; 2000US-0215135.
; 2000US-0216647.
; 2000US-0216880.
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2000US-0184668.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
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2000US-0217487

2000US-0217496

2000US-021963

2000US-0220963

2000US-0220964

2000US-0224518

2000US-0224519

2000US-0225214

2000US-0225214

2000US-0225266

2000US-0252667

2000US-025276

2000US-025276

2000US-025277
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2000US-0214886.
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Pred. No. 1.9e+02;
0; Mismatches 1
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    05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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18-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
 29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CT-2000;
20-NOV-2000;
20-NOV-2000;
08-NOV-2000;
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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14-SEP-2000;
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14-SEP-2000;
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12-SEP-2000;
14-SEP-2000;
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27-SEP-2000;
29-SEP-2000;
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  3-NOV-2000;

3-NOV-2000;
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2000US-0225759
2000US-0226279
2000US-0226681
2000US-0226868
2000US-0227109
2000US-0227009
2000US-0229287
2000US-0229287
2000US-0229287
2000US-0229343
2000US-0229344
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2000US-0231242.

2000US-0231244.

2000US-0231244.

2000US-0231244.

2000US-0231411.

2000US-023141.

2000US-0232080.

2000US-0232081.
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2000US-0233063.
2000US-0233064.
2000US-0233065.
2000US-0234223.
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2000US-0232397.
2000US-0232398.
  2000US-0241786.
2000US-0241808.
2000US-0241809.
2000US-0244619.
2000US-02446174.
2000US-02446174.
2000US-0246475.
2000US-0246476.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246528.
2000US-0246524.
2000US-0246524.
2000US-0246525.
2000US-0246528.
2000US-0246528.
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2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246528.
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2000US-0237039
2000US-023904
2000US-023994
2000US-0239937
2000US-0249937
2000US-0241986
2000US-0241785
2000US-0241786
2000US-0241786
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2000US-0236368
2000US-0236369
2000US-0236370
2000US-0236370
2000US-0236370
2000US-0237037
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2000US-0235484.
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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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2000US-0251030.
2000US-0251988.
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2000US-0249297.
2000US-0249299.
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2000US-0251990.
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2000US-0251869.
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2000US-0249218.
2000US-0249244.
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2000US-0249212.
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wound healing;

anti-HIV,

CA, Barash SC, Ruben SM;

2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 35824; 3071pp + Sequence Listing; English

proteins,

expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I) Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased sequences used in the exemplification of the present invention

Sequence 12710 BP; 3496 A; 2567 C; 2575 G; 4072 T; 0 other;

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Query Match
Best Local S
     Matches
              Similarity
   Conservative
            82.0%;
 0;
            Score 16.4; DB 22;
Pred. No. 2e+02;
   Mismatches
           2e+02;
                     Length 12710;
0; Gaps
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0

Best Local Similarity Matches 17; Conserv

Conservative

0; Mismatches Score 16.4; DB 25; Pred. No. 2e+02;

82.0%; 94.4%;

Length 12710;

<u>.</u>

Gaps

0;

Query Match

Sequence 12710 BP; 4072 A; 2575 C; 2567 G; 3496 T; 0 other;

S

2 GACAAGCCCTGACAAGCC 19

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RESULT 5
ABZ74552
ID ABZ74552
ID ABZ752
XX ABZ7
XX ABZ7
XX ABZ7
XX ABZ7
XX Huma
XW Auto
OX Homo
XW Acqu
KW Cyto
CX Homo
XX Homo
XX WO20
XX WO20
XX WO20
XX ABZ7
PP 26-N
XX X Z7-N
PR 12-6
PF 1
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                                                                                                  migration, prohormone activation and neurotransmitter activity. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing or treating cancers or other hyperproliferative disorders. Additionally, the secreted proteins and their nucleic acids may also be used in the treatment of autoimmune disorders, inflammatory disorders, diseases involving angiogenesis, AIDS (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein genomic fragment referred to in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted protein genes, and ABP00947-ABP01363 represent the protein genes, and ABP00947-ABP01363 represent the protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins the use of the secreted proteins in drug screening and recombinant vectors and host cells comprising a nucleic acid of the invention. The secreted proteins are thought to be involved in biological activities associated with cellular signalling, cellular differentiation, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 2278-2281; 2474pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human secreted proteins and nucleic acids, useful for detecting or treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia -
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12-SEP-2001; 2001US-0950082.
12-SEP-2001; 2001US-0950083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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N

GACAAGCCCTGACAAGCC

19

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RESULT 6
ABX52814/c
ID ABX528
XX Bovine
XX Bovine
XX Bovine
XX Bovine
XX Bovine
XX US2002
XX US2002
XX 17-DEC
PR 15-DEC
XX (BYAT)
PA (MATH)
PA (MARN)
PA (MA
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                                                                                                 CC from cattle, and the LMFD nucleic acid can specifically hybridise to a compunence, appearing as ABX50072-ABX55983, or complements of them. CC Also included are; (1) a transformed cell having a nucleic acid comprising an included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-cc transcription and addition of polyadenylated ribonucleotides to a 3' end comprising an addition of polyadenylated ribonucleotides to a 3' end complement and comprising any of the 5912 nucleic acid sequences or its complement of transcription and addition of polyadenylated ribonucleotides to a 3' end complement acid (comprising any of the 5912 nucleic acid sequences or its complement from the bovine cell or tissue comprising; (a) incubating a marker complement from the bovine cell or tissue, where hybridisation between the complementary nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is used for detection of the complementary nucleic acid is used for determining a level or pattern of the complementary gene identification and analysis, cantle breeding, preparation of compositions for use in cattle gene expression, or for genome compositions and complement sequence is one of the 5912 bovine composition that the complement sequence is one of the 5912 bovine composition that the sequence is one of the sequence that the composition between the composition and analysis, cantle breeding, preparation of improving cattle. The present sequence is one of the 5912 bovine composition that the composition but the sequence is one of the sequence that the composition but the sequence that the sequence is one of the sequence that the composition but the sequence that the sequence the sequence that the sequence that 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purified nucleic acid molecules, useful for genome mapping, identification and analysis, cattle breeding or preparation constructs for cattle gene expression and genetically impro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Byatt JC,
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15-DEC-1999;
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                                    Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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99US-0465231.
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ARRESULT 7

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03-DEC-1997;
09-SEP-1998;
                                                              in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GM4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences

AEXI7942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding human GM4,6D peptides of the invention.

Note: The sequence data for this patent did not form part of the printed appecification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cellular fucosylation; glycoconjugate fucosylation; transplant rejarthritis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 433 BP; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a composition comprising a human GDP-mannose, 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation in the composition of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
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98US-0149674.
99US-0333177.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins ar antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention.
                          08-OCT-1999
                                                                             AAZ11974;
                                                                                                                              AAZ11974 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 261 BP; 53 A; 71 C; 65 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 746; 815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-2001; 2001GB-0003424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N. gonorrhoeae nucleotide sequence SEQ ID 7651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fontana MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2002; 2002WO-IB02069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200279243-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria gonorrhoeae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; infection; vaccine; gene therapy; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABZ41531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABZ41531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-058415/05.
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                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                            2 GACAAGCCCTGACAAGCCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
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                                                                                                                                                                                                                                                            GACAAGCCTTGCCAAGCCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACAAGCCCTGACAAGCC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; 261 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACAAGCTCGGACAAGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pizza M,
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                          (first entry)
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                                                                                                                              DNA; 273
                                                                                                                                                                                                                                                                                                                                                                                  79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; 66 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%;
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                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
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Pred. No. 2.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8; DB 25;
                                                                                                                                                                                                                                                                                                                                                                                       Pred.
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                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monaci
                                                                                                                                                                                                                                                                                                                                                                                       2.4e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ħ
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 261;
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06-NOV-1997;
14-NOV-1997;
                                                                                             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septi
                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful
                                                                                   antibacterial;
                                                                                                                                 Neisseria meningitidis ORF 091 partial DNA sequence SEQ ID NO:307
                                                                                                                                                              21-MAR-2000
                                                                                                                                                                                     AAZ53178;
                                                                                                                                                                                                            AAZ53178 standard; DNA; 288
                                                                                                                                                                                                                                                                                                                                                                        Sequence 273 BP; 75 A; 67 C;
                                                                                                                                                                                                                                                                                                                                                                                               as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 61; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LO-DEC-1997
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                                                                                                                                                                                                                                                                           217
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                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                        GACAAGCCTTGCCAAGCCA
                                                                                                                                                                                                                                                                                                 GACAAGCCCTGACAAGCCA
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                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                           (first entry)
                                                                                 gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97GB-0024386.
97GB-0025158.
97GB-0026147.
98GB-0000759.
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97GB-0023516.
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                                                                                                                                                                                                            ВP
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                                                                                                                                                                                                                                                                        199
                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 20
Pred. No. 2.4e+02
                                                                                                                                                                                                                                                                                                                                                                        83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z,
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                        48 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                 DB 20;
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                                                                                              septicaemia;
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11-NOV-1999

WO9957280-A2

Neisseria meningitidis

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AAZ53176
ID AAZ5
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Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 287; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY74416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 288 BP; 57 A; 73 C; 74 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   Neisseria gonorrheae ORF 091 partial DNA sequençe SEQ ID NO:303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ53176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ53176 standard; DNA; 309 BP
                                                                                                                                                                                                                                                                        Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2000 (first entry)
                               30-APR-1999;
                                                                                    11-NOV-1999.
                                                                                                                                        WO9957280-A2
                                                                                                                                                                                            Neisseria gonorrheae
                                                                                                                                                                                                                                                antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GACAAGCCCTGACAAGCCA 20
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Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0083758.
98US-0094669.
98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
98US-0103796.
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                                                                                                                                                                                                                                                   gene therapy; ds.
                                  99WO-US09346.
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89.5%;
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Pred. No. 2.
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Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.4e+02; |
ches 2;
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Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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 RESULT 12
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31-JUL-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to meanufacture of medicaments for treating or preventing infection due to meanufacture of Neisseria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves be used to screen for agonists or antagonists, which may themselves be used as antibacterial agents. The polynucleotides of the invention have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polymucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473. The PCR primers used in the exemplification of the present invention. The pcr primers used in the exemplification of the present inventions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 287; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel Neisserial polypeptides predicted to be useful antigens for
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Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY74414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 309 BP; 64 A; 82 C; 78 G; 85 T; 0 other;
01-SEP-1998;
06-NOV-1997;
14-NOV-1997;
                                                                                                                                                                                                                                 Neisseria gonorrhoeae complete ORF37 sequence.
                                                                                                                                                                                                                                                                                               AAZ11975;
                                                                                                                                                                                  Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.
                                                                                                                                                                                                                                                                  08-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                               AAZ11975 standard; DNA; 381 BP
                                                                                                                           WO9924578-A2
                                                                                                                                                      Neisseria gonorrhoeae.
                                                             09-OCT-1998;
                                                                                             20-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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17; Conserv
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, Pizza M, Rappuoli R,
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98US-0098994.
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99US-0121528.
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   98GB-0019016.
97GB-0023516.
97GB-0024190.
                                                               98WO-IB01665
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89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Ratti G,
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Scalato E, §
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RESULT 13
AAK58992
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Best Local (
                          28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                       19-MAY-2000;
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17-MAR-2000;
                                                                                                                                                                                                                        24-FEB-2000;
02-MAR-2000;
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04-FEB-2000;
                                                                                                                                                                        18-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                     WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:4052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK58992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 381 BP; 106 A; 84 C; 114 G; 77 T; 0 other;
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27-NOV-1997;
10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY38502.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JAN-1998;
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Similarity 89.5%;
                        2000US-0209467
2000US-0214986
2000US-0215135
2000US-0216647
2000US-0216880
2000US-0217487
2000US-0217496
                                                                                                                                              2000US-018464.

2000US-0186350.

2000US-019974.

2000US-019076.

2000US-019123.

2000US-0205515.
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2000US-0180628
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97GB-0025158.
97GB-0026147.
98GB-0000759.
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Pred. No. 2.5e+02;
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20-OCT-2000
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21-SEP-2000; 2
25-SEP-2000; 2
25-SEP-2000; 2
25-SEP-2000; 2
25-SEP-2000; 2
27-SEP-2000; 2
27-SEP-2000; 2
27-SEP-2000; 2
29-SEP-2000; 2
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08-SEP-2000;
08-SEP-2000;
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06-SEP-2000;
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08-SEP-2000;
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22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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01-SEP-2000;
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01-SEP-2000;
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14-AUG-2000;
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26-JUL-2000;
26-JUL-2000;
2000US-0240960
2000US-0241785
2000US-0241785
2000US-0241787
2000US-0241787
2000US-0241808
2000US-0241808
2000US-0241808
2000US-0241806
2000US-0241826
2000US-0241826
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2000US-0231413

2000US-0231414

2000US-0232081

2000US-023298

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2000US-0232400

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2000US-0234274

2000US-0234283

2000US-0234884

2000US-0235884

2000US-0235886

2000US-0236367

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2000US-02363703

2000US-0237039
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2000US-0239935.
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2000US-0229343
2000US-0229344
2000US-0229345
2000US-022939
2000US-022950
2000US-0229513
2000US-0230437
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2000US-0226868.
2000US-0227182.
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2000US-0225447.
2000US-0225757.
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2000US-0231242.
2000US-0231243.
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2000US-0220963.
2000US-0220964.
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2000US-0228924
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921; (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient s genome that affect the activity of (I) by expressing inactive proteins or to pupplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (II) by inserting the minimal activity of the secreted (II) by inserting the minimal activity of the secreted (II) and the sec
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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01-DEC-
                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 4052;
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                                                                                                                                                                                                                                                                                                                                                                                                             Rosen
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08-DEC-2000;
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2000;
08-NOV-2000;
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      nucleic acids into a host cell
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2000US-0249209

2000US-0249209

2000US-0249210

2000US-0249211

2000US-0249211

2000US-0249212

2000US-0249213

2000US-0249215

2000US-0249216

2000US-0249216

2000US-0249218

2000US-0249218

2000US-0249218

2000US-0249244

2000US-0249244

2000US-0249264

2000US-0249264

2000US-0249264

2000US-0249264

2000US-0249299

2000US-0250391

2000US-0251988

2000US-0251869

2000US-0251869
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2000US-0246609.
2000US-0246610.
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2000US-0246475.
2000US-0246476.
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2000US-0246528.
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RESULT 14
AAK74242
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Matches
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                                                                                                                            14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                 18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                             14-AUG-2000;
14-AUG-2000;
                                                                    14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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26-JUL-2000;
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                                                                                                                                                                                                                                                                         28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                     16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; gene therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK74242 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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        2000US-0189874.
2000US-0190076.
2000US-0198123.
2000US-0209467.
2000US-0214886.
2000US-0216647.
2000US-0217496.
2000US-0217496.
2000US-0218290.
2000US-0218290.
2000US-0218291.
2000US-022954.
2000US-0225214.
2000US-0225267.
2000US-0225567.
2000US-0225759.
2000US-02256868.
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2000US-0180628
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2000US-0186350.
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89.5%;
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Pred. No. 2.5e+02
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 409;
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23-AUG-2000; 30-AUG-2000; 01-SEP-2000;

2000US-0227009. 2000US-0228924. 2000US-0229287. 2000US-0229343.

2000US-0229513. 2000US-0230437.

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RESULT 15
AAK74243
                                                                                                                                                                                                                               CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cC artivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynuclostides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC supplement the patients own produce the secreted (I), by inserting CC polynucleotides may be used to produce the secreted (I), by inserting CC protein. (I) proteins and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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                                                                                                                                                       Matches
                                                                                                                                                                       Query Match
Best Local
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17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249213.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249214.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0259390.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251479.
06-DEC-2000; 2000US-0251866.
08-DEC-2000; 2000US-0251866.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0251999.
08-DEC-2000; 2000US-0251999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _{\rm Nucreic} acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                               Sequence 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 29054; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                           558 GGACATGCCCGGACAAGCC 576
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                                                                                                                                                       17;
                                                                                                                                                                       Similarity
                                                                                                                 GGACAAGCCCTGACAAGCC 19
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                 BP; 201 A; 185 C; 137 G; 226 T; 0 other;
                                                                                                                                                                       79.0%;
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                                                                                                                                                                       Score 15.8; DB 22;
Pred. No. 2.7e+02;
                                                                                                                                                         Mismatches
                                                                                                                                                           Indels
                                                                                                                                                                                             Length 749;
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                                                                                                                                                         Gaps
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29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 02-OCT-2000; 02-OCT-2000;

14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000;

14-SEP-2000;

2000US-0231438.
2000US-0231243.
2000US-0231244.
2000US-0231414.
2000US-0231414.
2000US-0231498.
2000US-023298.
2000US-0232397.
2000US-0232400.
2000US-0232400.
2000US-0233401.
2000US-0233401.
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2000US-0233401.
2000US-0233401.
2000US-0233401.
2000US-0233441.
2000US-0233441.
2000US-023424.
2000US-023424.
2000US-023424.
2000US-023424.
2000US-0234274.
2000US-0234284.
2000US-0234284.
2000US-0234284.
2000US-02343834.
2000US-02343834.
2000US-02343834.
2000US-02343834.
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2000US-02343834.
2000US-02343834.
2000US-02343834.
2000US-02343834.
2000US-02343837.
2000US-02343637.
2000US-0234634.

27-SEP-2000;

02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 13-OCT-2000; 13-OCT-2000; 20-OCT-2000;

2000US-0237038. 2000US-0237039. 2000US-0237040.

2000US-0239935. 2000US-0239937. 2000US-0240960. 2000US-0241221. 2000US-0241785. 2000US-0241785. 2000US-0241787.

20-OCT-2000; 01-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

3-NOV-2000;

2000US-0241808.
2000US-0241809.
2000US-0244617.
2000US-0246474.
2000US-0246476.
2000US-0246476.
2000US-0246477.
2000US-0246523.
2000US-0246524.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246513.
2000US-0246613.
2000US-0246613.
2000US-0249209.

08-NOV-2000;

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	UXXXXI
Humani immune/haematopoletic; immune/haematopoletic; immune/haematopoletic; immune/haematopoletic; immune/haematopoletic antigen; cancer; cyrcetatic; gene therapy; vaccine; metastasis; ds.	AAK74243 standard; DNA; 749 BP. AAK74243; 07-NOV-2001 (first entry)
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21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-OCT-2000; 02-OCT-2000; 03-NOV-2000; 04-NOV-2000; 06-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 01-NOV-2000; 08-NOV-2000; 01-NOV-2000; 01-NO	-SEP-2000; -SEP-2000; -SEP-2000; -SEP-2000;
2000US-0234054 2000US-0234223 2000US-0234297 2000US-0234994 2000US-0235834 2000US-0235834 2000US-0235363 2000US-0236327 2000US-0236327 2000US-0236327 2000US-0236327 2000US-0236327 2000US-0237039 2000US-0237039 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241808 2000US-0241787 2000US-0241808 2000US-0241821 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246476 2000US-0246471 2000US-0246471 2000US-0246471 2000US-0246471 2000US-0246471 2000US-0246471 2000US-0246471 2000US-0246471 2000US-0246471 2000US-0246471 2000US-0246471 2000US-024671 2000US-024671 2000US-024671 2000US-024671 2000US-024671 2000US-024671 2000US-024671 2000US-024671 2000US-024671 2000US-0249211 2000US-	023

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Search completed: August 1, 2003, 13:55:23 Job time: 6.69868 secs
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                                                                                                                                                                                                                                                                         CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (II, by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK875950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
                                                                                                                                                                 Query Match
Best Local S
Matches 17
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06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0251990.
05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                             Sequence 749 BP; 201 A; 185 C; 137 G; 226 T; 0 other;
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                                                                                                                                                                 Local Similarity hes 17; Conserv
                                                                                  558 GGACATGCCCGGACAAGCC 576
                                                                                                                      1 GGACAAGCCCTGACAAGCC 19
                                                                                                                                                                   Conservative
                                                                                                                                                                                  79.0%; Score 15.8; DB 22; Length 749; 89.5%; Pred. No. 2.7e+02;
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                                                                                                                                                               0;
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                                                                                                                                                               2; Indels
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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                              18.4
16.8
16.8
16.8
16
15.8
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20
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/ cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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7955.924 Million cell updates/sec
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Sequence 24, Appl
Sequence 32, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
     Sequence 9, Appli
Sequence 174763,
Sequence 1101, Ap
Sequence 2743, Ap
Sequence 9518, Ap
Sequence 87503, A
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## ALIGNMENTS

US-09-834-291-5

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Sequence 10, Application US/09834291
patent No. US20020042064A1
GENERAL INFORMATION:
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US-09-834-291-5
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                                                   RESULT 2
US-09-834-291-10
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Patent No. US20020042064A1
                                                                                                                                                                                                                                                                                               SEQ ID NO 5
LENGTH: 2
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1999-10-16
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                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 32
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APPLICANT: Krammer, Peter

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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Ozen, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR APPLICATION NUMBER: D5 198 47 779.1
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-10-16
VOUMBER OF SEQ ID NOS: 32
SEQ ID NO 24
TENCRUS. 24
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                                                                                                                                                                     GENERAL INFORMATION:
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               APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE *KEFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
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FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT ETLING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1998-10-16
PRIOR APPLECATION NUMBER: PCT/DE99/03343
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SEQ ID NO 10
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ORGANISM: Homo Sapiens
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CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                             US-09-834-291-3
; Sequence 3, Application US/09834291
; Patent No. US20020042064A1
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APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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US-09-834-291-32
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                                                                                                                                                                      TITLE OF INVENTION: p53 Binding Areas
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Patent No. US20020042064A1
LENGTH: 2380
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 266
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TYPE: DNA
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TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
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APPLICANT: Muller-Schilling, Martina
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PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
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100.0%; Pred. No. 1
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TYPE: DNA

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                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Wuller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/0343
PRIOR APPLICATION NUMBER: DE 1898 47 779.1
PRIOR APPLICATION NUMBER: DE 1988 47 779.1
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TITLE OF INVENTION: p53 Binding Areas
TITLE REFERENCE: 4121-122
FILE REFERENCE: 4121-122
FURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION UNDEER: DE 198 47 779.1
PRIOR APPLICATION UNDEER: DE 198 47 779.1
PRIOR FILING DATE: 1999-10-16
PRIOR FILING DATE: 1999-10-16
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Best Local Similarity
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Patent No. US20020042064A1
                                                                                                                                          PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 1
LENGTH: 3212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Krammer, Peter APPLICANT: Muller-Schill: APPLICANT: Oren, Moshe
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                                   Query Match
Matches
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ORGANISM: Homo Sapiens
                                                                                                        ORGANISM: Homo Sapiens
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  Local Similarity
hes 20; Conserv
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100.0%; Score 20; DB nilarity 100.0%; Pred. No. 1.2; Conservative 0; Mismatches
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                                              DB 9; 'Length 3212;
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US-09-834-291-6
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CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING TOTAL TOTA
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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
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NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                Query Match
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PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: D53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 20
TYPE: DNA
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Local Similarity 95.0%; Pred. No. 7.4;
hes 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                             0; Mismatches
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RESULT 11

US-09-834-291-9

Sequence 9, Application US/09834291 Patent No. US20020042064A1

GENERAL

INFORMATION:

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APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
                                             Matches
                                                                                   Query Match
                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 174763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION IDEATE: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
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                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(2940917)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                       ORGANISM: Human FEATURE:
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                                                                                                                                                                                                                                                     TYPE: DNA
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                                                               Local Similarity
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APPLICATION NUMBER: US 60/167,363
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                                         18; Conservative
1 GGACAAGCCCTGACAAGCCA 20
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                                                      84.0%; Score 16.8;
90.0%; Pred. No. 46
                                   0; Mismatches
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                                                                      DB 13; Length 2940917;
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TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(516)

OTHER INFORMATION: n = A,T,C or G

US-09-728-444-1101
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                                                                                                                                              NUMBER OF SEQ ID NOS: 5912

SEQ ID NO 2743

LENGTH: 433

TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
OTHER INFORMATION: Clone ID: 13-LIB3058-025-Q1-K1-D1
                                                                                                                                                                                                                                                                               APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Hathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 37-21(10297)C
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US/09/983,965
PRIOR APPLICATION NUMBER: US/09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1998-12-17
                                                  Matches
                                                                                          Query Match
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APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. US20020161207A1el Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0100-USA
CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION UNMBER: US 60/168,360
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1206
SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1101
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Patent No. US20020161207A1
GENERAL INFORMATION:
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                                                                  Local Similarity
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4 CAAGCCCTGACAAGCC 19
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100.0%; Pi
                                                         80.0%; Score 16; DB 10; 100.0%; Pred. No. 1.2e+0;
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94.4%; Pred. No. 74;
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                                          Mismatches
                                                             1.2e+02;
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RESULT 15

US-09-878-574-9518

Sequence 9518, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT PAPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION UNUMBER: 09/333,535

PRIOR APPLICATION UNUMBER: 09/333,535

PRIOR APPLICATION UNUMBER: 09/33,535

FILOR OF SEQ ID MOS: 15775

SEQ ID NO 9518

LENCTH: 165

TYPE: DNA

ONGANISM: Glycine max

OTHER INFORMATION: Clone ID: 701102580H1
Search completed: August 1, 2003, 13:37:14 Job time : 17.1861 secs
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                                                                                                                                                                                      Query Match 79.0%; Score 15.8; DB 10; Best Local Similarity 89.5%; Pred. No. 1.5e+02; Matches 17; Conservative 0; Mismatches 2;
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131 GGACAAGCTCGGACAAGCC 149
                                                                                                                                                                                                                                    Length 165;
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Perfect score:
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Maximum DB seq length: 200000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Listing first 45 summaries
                                      GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-460-309-3

US-08-125-077-3

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US-09-252-991A-8300

US-09-252-991A-8306

US-09-254-905-221

US-09-564-805-221

US-09-315-127-4

US-09-315-127-4

US-08-311-71A-120

US-08-311-71A-120

US-08-317-35

US-08-347-792-18

US-08-347-792-18

US-08-347-792-18

US-08-397-221-29

US-08-397-221-29

US-08-397-231-29

US-08-397-331

US-08-687-227-31

US-08-687-237-31

US-08-687-237-31

US-08-687-237-31

US-08-687-231-29

US-08-99-327-31

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US-08-460-309-1
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5347.959 Million cell updates/sec
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Sequence 3, Appli
Sequence 5635, Ap
Sequence 113, App
Sequence 8300, Ap
Sequence 8306, Ap
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Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5444158
                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                          Sequence 120, App
Sequence 35, Appl
Sequence 35, Appl
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Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 5, Appri	1 1			7 5			Seguence 68, Appl	Sequence Loose, A		1	28	Seguence 3, Appli	sequence o, Appri	,		Seguence 86, Appl	Sequence 93, Appl

## ALIGNMENTS

RESULT 1 US-09-220-132-85

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US-09-220-132-85
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US-08-460-309-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 85, Applicate Patent No. 6506607
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 07334-074001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
PRIOR FILING DATE: 1997-12-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1997-1
NUMBER OF SEQ ID NOS: 191
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 1923
                                                                                                                                                                                     APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
                                                                                                                                               NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                      STREET: 4370 La Jolla Village
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                         1572 GCANAGGCCCTGACAAGCCA 1591
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                                                                                                                             Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%; Score 15.2;
85.0%; Pred. No. 77;
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                                                                                                             Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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MEDIUM TYPE:

Floppy disk

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RESULT 3
US-08-125-077-1
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Patent No. 5872231
Patent No. 5872231 5840863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3554 back
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CAPPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-UTL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TRILERAY: (610) 635-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                  San Diego
: California
                                                                                                                                                                                                                                          E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                      USA
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SYSTEM: PC-DOS/MS-DOS
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US-08-460-309-3
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; NAME/KEY:
; LOCATION:
US-08-125-077-1
                                                                                                                                                                                                                                                                                                                                                      5444158-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATENT NO. 5444158
APPLICANT: ENGVALL, EVA; SANES, JOSHUA
TITLE OF INVENTION: MEROSIN, NUCLEIC ACIDS ENCODING,
FRAGMENTS AND USES THEREOF
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
5444158-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   뭉
                                                                           Sequence 3, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                  Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/87
FILING DATE: 08-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 587,689
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 472,319
FILING DATE: 30-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/107
FILLING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
       APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nuc
TITLE OF INVENTION: Fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3554
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                                                                                                                                                                                                     183 GGACAAAGCCAGACAAGCCA 202
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                                                          Eva
Nucleic Acids Encoding Merosin, Merosin Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                            76.0%; Score 15.2;
85.0%; Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/87,642
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                       DB 6; Length 3554;
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; Sequence 3, Application US/08125077; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
   APPLICANT: Engvall, Eva
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FILING DATE: 21-SEP-194

PRIOR APPLICATION UNMEER: US 07/472,319

APPLICATION NUMEER: US 07/472,319

FILLING DATE: 30-JAN-1990

PRIOR APPLICATION NUMEER: US 07/919,951

APPLICATION NUMBER: US 07/919,951

FILLING DATE: 27-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,915

REFERENCE/DOCKET NUMBER: 91,915

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9091

TELEPAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                    APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 45..
STREET: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                          STREET: SAN Diego CITY: San Diego STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/125,077
PILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/460,309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match
Local Similarity 85.0%;
hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 6942 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                        COUNTRY:
                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6163 GGACAAAGCCAGACAAGCCA 6182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                    E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
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Pred. No. 96;
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; Sequence 113, Application US/09489847

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Sequence 5635, Application US/09252991A

PALENT NO. 6551795

GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FULL REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
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US-09-252-991A-5635/c
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RESULT 8
US-09-489-847-113
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                                                                                                                                                                                                                                                                                 SEQ ID NO 5635
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5635
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      Matches
                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/125,077 FILING DATE: 22-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Campbell, Cathryn A REGISTRATION NUMBER: 31,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                            67 GGACAAGCAGTGACAAGC 50
                                                                                                                                                                                                                                                                                     1185
                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n 76.0%; Score 15.2; Similarity 85.0%; Pred. No. 96
                                                                                                                1 GGACAAGCCCTGACAAGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 6942 base pairs nucleic acid
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                                                                                                                                                                        74.0%; Score 14.8; DB 4; Length 1185; 88.9%; Pred. No. 1.1e+02;
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                                                                                                                                                            Mismatches
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GENERAL INFORMATIO

INFORMATION:

APPLICANT: Rosen et al

FILE REFERENCE: PZ031P1

TITLE OF INVENTION: 98 Human Secreted Proteins

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RESULT 10
US-09-252-99]A-8306
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                                                                                                                                                                                                                                                      US-09-252-991A-8300
                                                                                                                                                                                                                                                                                                                                               FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-8300
                                                                                                                                                                                                                                                                 SEQ ID NO 8300
LENGTH: 360
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                            Matches
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8300, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-07-30
EARLIER FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (289)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1998-08-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 2214
                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                    245 CAAGCGCTGACAAGCC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 GGGRARGGCCTGACAAGCCA 324
                                                                                                                           4 CAAGCCCTGACAAGCC 19
                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Conservative
                                                                                                                                                                    Conservative
                                                                                                                                                                            72.0%; Score 14.4; DB 4; Length 360; 93.8%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%;
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Pred. No. 1.
                                                                                                                                                               Mismatches
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; TOPOLOGY: linear US-08-240-372-1
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US-08-240-372-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8306
                  Matches
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Patent No.
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/240, FILING DATE: 10-MAY-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MURASHIGE, KATE H. REGISTRATION NUMBER: 29,959 REFERENCE/DOCKET NUMBER: 3918. TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                                       TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08240372 Patent No. 5741665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: KATO, ELIE K.

APPLICANT: STUART, W. DORSEY

APPLICANT: STUART, W. DORSEY

TITLE OF INVENTION: LIGHT-REGULATED PROMOTERS FOR PRODUCTION

TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS IN FILAMENTOUS FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SEQ ID NO 8306
LENGTH: 417
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8306, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                TELEPHONE: (202) 887-0763
                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OCTEMATING SYSTEM: PC-DOS/MS-DOS
DEBENT: PatentIn Dalan
                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 CAAGCGCTGACAAGCC 317
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                                                                                                                                                                 1237 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: MORRISON & FOERSTER 2000 Pennsylvania Ave. N.W.
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    unueR: US/08/240,372
10-MAY-1994
72.0%; Score 14.4; DB 1; Length 1237; 93.8%; Pred. No. 1.9e+02; ctive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.0%; Score 14.4; DB 4; Length 417; 93.8%; Pred. No. 1.5e+02;
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
CORTEMBER: DESCRIPTION SECRIPTION SE
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; NAME/KEY: CDS
; LOCATION: (1)..(2466)
US-09-564-805-221
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                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1995-08-23
EARLIER FILING DATE: 1995-08-23
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: COllins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09011745 Patent No. 6165715
                                                                                                                                                                                                                                   SEQ ID NO 7
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Best Local Similarity
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                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver.
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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: construct
                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                            TYPE: DNA
                                                                      FEATURE:
                                                                                                                                                                                             ENGTH: 6312
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93.8%;
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Pred. No. 2.1e+(
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                                 Portion of
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US-09-315-127-4
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                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: The University of Tennessee, c/o Richard Cox
APPLICANT: The University of Tennessee, c/o Richard Cox
TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
FILE REFERENCE: 44137-5023, U. of Tennessee
CURRENT APPLICATION NUMBER: US/09/315,127
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09315127
Patent No. 6448390
                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:SEQ. OTHER INFORMATION: retroviral vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (4249)
OTHER INFORMATION: n is any nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (4246)
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                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                TYPE: DNA
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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                                                                                                                                                                                                                                                                                                             ENGTH: 8088
                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3115 CAAGGCCTGACAAGCC 3130
7121 CAAGGCCTGACAAGCC 7136
                                                                       15;
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                   4 CAAGCCCTGACAAGCC 19
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                                                                       Conservative
                                                                                       72.0%;
93.8%;
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                                                                                       Score 14.4; DB 4;
Pred. No. 2.6e+02;
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                                                                       Mismatches
                                                                                                      Length 8088;
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                                                                       Indels
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                                                                     Gaps
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US-08-716-351A-1
US-08-716-351A-1
Sequence 1. Application US/08716351A
Patent No. 603305
GENERAL IMPORMATION:
APPLICANT:
ITTLE OF INVENTION: Gibbon Ape Leukemia Virus-Based
ITTLE OF INVENTION: Gibbon Ape Leukemia Virus-Based
ITTLE OF INVENTION: Retroviral Vectors
COMPUTER REDAMLE FORM.
MEDIUM TYPE: Ploppy disk
COMPUTER REDAMLE FORM.
MEDIUM TYPE: NUMBER: US/08/716,351A
PILLOCATION NUMBER: US/08/716,351A
PILLOCATION NUMBER: US/08/716,351A
PILLOCATION NUMBER: US/08/716,351A
PRICACTION NUMBER: US/08/716,351A
PRICACTION NUMBER: US/08/716,351A
PRICACTION TOR SEQUENCE CHARACTERLSTICS:
LENGTH: 835 base pairs
SEQUENCE CHARACTERLSTICS:
LENGTH: 835 base pairs
TYPE: mucleic acid
STRANDENESS: single
OFFICE TYPE: DNA (genomic)
PEATURE:
LENGTH: 835 base pairs
TYPE: mucleic acid
STRANDENESS: Single
OFFICE TYPE: DNA (genomic)
PEATURE:
LOCATION: 1. 1835 b
OFFICE TYPE: Misc feature
LOCATION
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Result
No.
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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20
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
 ggacaagccctgacaagcca 20
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                                                                                                                                         US-08-460-309-3

US-08-125-077-3

US-09-252-991A-5635

US-09-252-991A-8306

US-09-252-991A-8306

US-09-252-991A-8306

US-09-252-991A-8306

US-09-264-805-221

US-09-311-74-7

US-09-315-127-4

US-09-311-731A-120

US-08-311-731A-120

US-08-312-731A-120

US-08-312-731A-120

US-08-311-731A-120

US-08-312-73-31

US-08-32-542-31

US-08-392-542-31

US-08-392-542-31
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US-08-460-309-1
US-08-125-077-1
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                                                                                                                                                                                                                                                                                                 Sequence 85, Appl
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5444158
                                                                                                                                                                                                                       Sequence 3, Appli
Sequence 3, Appli
Sequence 5635, Ap
Sequence 113, App
Sequence 8300, Ap
Sequence 8306, Ap
                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                         Sequence
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Sequence
                                       Sequence
Sequence
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Sequence
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                            Sequence
                                                                Sequence
                                                                                                      Sequence
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                                                                                                                                                      7, Appli
4, Appli
1, Appli
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35,
35,
18,
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1, App
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71.0	71.0	71.0		71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0
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US-09-198-452A-1	US-08-125-077-3	US-08-460-509-5	10 00 100 00 00 00 00 00 00 00 00 00 00	US-08-726-214-5	US-08-894-997-49	US-09-620-312D-571	US-09-220-132-16	US-09-252-991A-10524	US-09-252-991A-10432	US-09-247-155-68	US-09-252-991A-10642	US-09-216-393H-L1	US-08-445-909A-28	US-09-577-640-3	US-08-9/9-586-3	US-09-312-283C-86	US-09-188-930-86	US-09-276-531-93
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## ALIGNMENTS

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RESULT 1
US-09-220-132-85
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; ORGANISM: Homo sapiens
US-09-220-132-85
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US-08-460-309-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 85, Application US/09220132
Patent No. 6506607
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: I
                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.0%; Score 15.2; Best Local Similarity 85.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shyjan, Andrew W.

APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 07334-074001

CURRENT APPLICATION NUMBER: US/09/220,132

CURRENT FILING DATE: 1998-12-23

PRIOR APPLICATION NUMBER: US 60/079,303

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: US 60/068,821

PRIOR PILING DATE: 1997-12-24

PRIOR FILING DATE: 1997-12-24

PRIOR FILING DATE: 1997-12-24

PRIOR FILING DATE: 1997-12-24
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                                                                                                                                                                                APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids
TITLE OF INVENTION: Fragments and
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 1923
                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
COMPUTER READABLE FORM:
                        COUNTRY: U
                                                              STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1572 GCAAAGGCCCTGACAAGCCA 1591
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                                               USA
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Uses Thereof
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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US-08-125-077-1
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PILLING DATE: 30-JAN-1990
PRIOR APPLICATION NUMBER: US 07/919,951
APPLICATION NUMBER: US 07/919,951
FILLING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENTOTUL 1254 hors mainly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08125077
Patent No. 5872231
Patent No. 5872231 5840863
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.0%; Pred. No. 86
Matches 17; Conservative 0; Mismatche
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                              STREET: 43, CONTROL STREET: 43, CONTROL SAN DIEGO CTATE: California
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA.

PRIOR APPLICATION NUMBER: US 08/125,077

PILING DATE: 22-SEP-1993

APPLICATION NUMBER: US PCT/US 94/10730

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                  ZIP: 92122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/460,309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 GGACAAAGCCAGACAAGCCA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGACAAGCCCTGACAAGCCA 20
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RESULT 5
US-08-460-309-3
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US-08-125-077-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ENGVALL, EVA; SANES, JOSHUA
TITLE OF INVENTION: MEROSIN, NUCLEIC ACIDS ENCODING,
FRAGMENTS AND USES THEREOF,
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Patent No.
                                                                                              Sequence 3, Application US/08460309 Patent No. 5837496
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
   GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucl
TITLE OF INVENTION: Frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/87
FILING DATE: 08-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 587,689
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 472,319
FILING DATE: 30-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3554 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: P. TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3554 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-JAN-1990
                                                                                                                                                                                                         183 GGACAAAGCCAGACAAGCCA 202
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                                                                                                                                                                                                                                            1 GGACAAGCCCTGACAAGCCA 20
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10..3400
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                                                                                                                                                                                                                                                                                              76.0%; Score 15.2;
85.0%; Pred. No. 8
Nucleic Acids Encoding Merosin, Merosin Fragments and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 07/919,951
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                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                 96;
                                                                                                                                                                                                                                                                                                           DB 6; Length 3554;
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US-08-125-077-3
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                                                                                                                                            Patent NO. JOYLE OF SEOUENCES: 23
                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08125077 Patent No. 5872231 Patent No. 5872231 5840863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.0%;
Best Local Similarity 85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/472,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILLING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6942 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                6163 GGACAAAGCCAGACAAGCCA 6182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGACAAGCCCTGACAAGCCA 20
                                                            92122
                                                                                        SSEE: Campbell and Flores
T: 4370 La Jolla Village Drive, Suite 700
San Diego
San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.2;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6942;
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; Sequence 113, Application US/09489847

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RESULT 8
US-09-489-847-113
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                                                                                                                                                                                                                                   ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-5635
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                                                                                                                                                                                                                                                                       ; SEQ ID NO 5635
; LENGTH: 1185
; TYPE: DNA
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                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/4
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/9
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P-LA 9721 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6942 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US PCT/US 94/10730 FILING DATE: 21-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6163 GGACAAAGCCAGACAAGCCA 6182
                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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                                                                                                                   1 GGACAAGCCCTGACAAGC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 76.0%;
Similarity 85.0%;
                                                                               GGACAAGCAGTGACAAGC 50
                                                                                                                                                       Conservative
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                                                                                                                                                                         74.0%; Score 14.8; DB 4; 88.9%; Pred. No. 1.1e+02;
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Pred. No. 9
                                                                                                                                                         Mismatches
                                                                                                                                                                                             DB 4;
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                                                                                                                                                                                           Length 1185;
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US-09-252-991A-8300
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CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,455
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SEQ ID NO 8300
LENGTH: 360
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SEQ ID NO 113
LENGTH: 2214
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APPLICANT: Marc J.
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                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al TITLE OF INVENTION: 98 Human Secreted Proteins FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 376
                                                                                                                                                                                                                                                              TYPE: DNA
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LOCATION: (289)
OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                         Local
245 CĂĂĠĊĠĊTĠĂĊĂĂĠĊĊ 260
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                                                4 CAAGCCCTGACAAGCC 19
                                                                                              h 72.0%; Score 14.4; DB 4; Length 360; Similarity 93.8%; Pred. No. 1.5e+02; 15; Conservative 0; Mismatches 1; Indels
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Pred. No. 1.36
1; Mismatches
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1.3e+02;
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RESULT 10 US-09-252-991A-8306

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Query Match
Best Local Similarity
....hes 15; Conserva
                                                                                                 US-08-240-372-1
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                                                                                                                                TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1237 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08240372 Patent No. 5741665
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SEQ ID NO. 8306
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 39
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 417
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KATO, ELIE K.
APPLICANT: STUART, W. DO
TITLE OF INVENTION: LIGH
TITLE OF INVENTION: OF H
                                                                                                                                                                                                                                              ELECUTE: (202)
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Local Similarity 93.8%; Pred. No. 1.5e+02;
hes 15; Conservative 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                  TOPOLOGY:
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                                                                                                       linear
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORRISON & FOERSTER
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                                    72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIGHT-REGULATED PROMOTERS FOR PRODUCTION
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                  Score 14.4; DB 1;
Pred. No. 1.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                 3918-0003.00
                                                       Length 1237;
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                                                                                                                                                                                                APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 221, Apr-
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                                                                                                                                                                                    SEQ ID NO 7
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CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Sus
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mus musculus
                                          OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: construct
                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                             ENGTH: 6312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 72.0%; Score 14.4; DB 4;
Local Similarity '93.8%; Pred. No. 2.1e+02;
hes 15; Conservative 0; Mismatches 1
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; LCCATION: (4249)
; OTHER INFORMATION: n is any nucleotide
US-09-011-745-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-315-127-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09315127
Patent No. 6448390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.0%; Score 14.4; DB 3; Best Local Similarity 93.8%; Pred. No. 2.5e+02; Matches 15; Conservative 0; Mismatches 1;
                                           Matches
                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4
                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy FILE REFERENCE: 44137-5033, U. of Tennessee CURRENT APPLICATION NUMBER: US/09/315,127
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The University of Tennessee, c/o Richard Cox
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Artificial Sequence:SEQ. ID NO. 3, OTHER INFORMATION: retroviral vector
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OTHER INFORMATION: n is any nucleotide
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LOCATION: (4246)
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LOCATION: (4061)
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OTHER INFORMATION: n is
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LOCATION: (5552)..(7552)
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LOCATION: (4247)
                                                                                                                                                                                                                                                                                                                      ENGTH: 8088
                                                               Local Similarity
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  4 CAAGCCCTGACAAGCC 19
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                                           Conservative
                                                               72.0%;
93.8%;
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                                                               Score 14.4; DB 4;
Pred. No. 2.6e+02;
                                                Mismatches
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                                                                                   Length 8088;
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